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APPLICANT: Schmaier, Alvin H.
APPLICANT: Schmaier, Alvin H.
APPLICANT: Schmaier, Alvin H.
APPLICANT: Schmaier, Vongping
TITLE OF INVENTION: Modulation of Blood
TITLE OF INVENTION: With Kininogen Fragment
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seidel, Gonda, Lavorgna &
ADDRESSEE: Monaco, P.C.
STREET: 1800 Two Penn Center Plaza
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                      9,7
12,4
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                                            Sequence Seq
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Sequence 8
Sequence 2
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CITY: Philadelphia
COUNTY: U.S.A.

ZIP: 1910.2

COUNTY: U.S.A.

ZIP: 1910.2

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
COMPUTER: IBM FS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/193,114B

FILING DATE: 9 February 1994

CLASSIFICATION DATA:
APPLICATION NUMBER: U.S. Application
APPLICATION NUMBER: Serial No. 5472945 07/744,545

FILING DATE: 13 August 1991

ATTORNEY/AGENT INFORMATION:
MAME: Monaco, Daniel A.
FELECOMMUNICATION INFORMATION:
TELEFRANCE/COCKET NUMBER: 6056-137 CII
TELEFRANCE CALSTONE (215) 568-5549

TELEFRANCE/COMPACTERISTICS:
LENGTH: 117 amino acids

"VDD: neptide
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Pred. No. 4.9e-15;
US-09-617-302-8
US-09-617-302-10
US-09-269-731-6
US-08-76-014-2
US-08-460-512-5
US-08-460-512-5
US-08-481-435-12
US-08-481-435-12
US-08-481-435-12
US-08-481-435-12
US-08-481-435-12
US-08-481-435-12
US-08-481-435-12
US-08-415-751-12
US-08-415-751-12
US-08-415-751-12
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US-08-721-259-2
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Best Local Similarity
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US-08-193-114B-1
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       July 1, 2002, 16:18:01; Search time 35.15 Seconds (without alignments) 22.237 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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1 TLTHTITKLNAENNATFYFKIDNVKKARVQVV 32
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US - 08 - 483 - 926A - 11

US - 08 - 873 - 045 - 12

US - 09 - 019 - 485 - 2

US - 09 - 019 - 485 - 3

US - 09 - 011 - 486 - 9

US - 09 - 011 - 486 - 9

US - 09 - 011 - 480 - 9

US - 09 - 011 - 480 - 9

US - 09 - 011 - 480 - 9

US - 08 - 751 - 521 - 20

US - 08 - 751 - 359 - 11

US - 08 - 751 - 359 - 11

US - 08 - 751 - 146 - 11

US - 08 - 846 - 671 - 14

US - 08 - 845 - 530B - 36

US - 08 - 378 - 939 - 32

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US - 08 - 744 - 138 - 2

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US - 09 - 431 - 480 - 10
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                            - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Maximum DB :
                                                                                                                                                                        OM protein
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Gaps
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                                                                                                                                                                                                                                                                                    CTHER INFORMATION: Description of Artificial Sequence: Bradykinin; OTHER INFORMATION: analog
US-08-676-242-15
                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Patent No. 5834592
GENERAL INFORMATION:
APPLICANT: Corixa Corporation
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
TITLE OF ENVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 52; DB 2; Length 701;
Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                  Length 26;
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APPLICATION NUMBER: US/08/533,669A FILING DATE: 22-SEP-1995
CLASSIFICATION: 424
ATTONNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REGISCOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                                                                                                                                                                                                59.0%; Score 95; DB 4; I 100.0%; Pred. No. 9.1e-07; tive 0; Mismatches 0;
                CURRENT FILING DATE: 2000-07-16
EARLIER APPLICATION NUMBER: 60/000,096
EARLIER FILING DATE: 1995-06-09
EARLIER FILING DATE: 1995-06-07
EARLIER FILING DATE: 1996-06-07
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VET. 2.1
SOFTWARE: PATENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
    CURRENT APPLICATION NUMBER: US/08/676,242C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32,3%;
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ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0
Matches 19; Conservative
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Best Local Similarity 38.5
Matches 10; Conservative
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US-08-533-669A-16
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US-08-533-669A-16
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APPLICANT: The Regents of the University of Michigan
APPLICANT: Schmater, Alvin H.
APPLICANT: Hasan, Ahmed A.K.
TIME OF INVENTION: Bradykinin Analogs As Selective Thrombin Inhibitors
FILE REFERENCE: 8820-2 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
    Gaps
                                                                                                                                                                                                                                  APPLICANT: Jiang, Yongping
TITLE OF INVENTION:
APPLICANT: Jiang, Yongping
TITLE OF INVENTION: Modulation of Blood
TITLE OF INVENTION: Modulation of Blood
TITLE OF INVENTION: Pressure by Altering Bradykinin Levels
NUMBER OF SEQUENCE: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Temple University - Of the
ADDRESSEE: Commonwealth System of Higher Education
STREET: Building
CITY: Philadelphia
STARET: Pennsylvania
COUNTRY: U.S.A.
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  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTAIL: U.S.A.

ZIPE: 1912: 1912: 1012: COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb COMPUTER: IBM PS/2 SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06809
FILING DATE: 19910813
CLASSIFTCATION NUMBER: PCT/US92/06809
FILING APPLICATION DATA:
APPLICATION NUMBER: Serial No. 744,545
FILING DATE: 13 August 1991
ATTORNEY/AGENT INFORMATION:
NAME: MONGCO, Daniel A.
REGISTATION NUMBER: 30,480
REGISTATION NUMBER: 30,480
  0; Mismatches
                                             1 TLTHTITKLNAENNATFYFKIDNVKKARVQVV 32
                                                                  1 TLTHTITKLNAENNATFYFKIDNVKKARVQVV 32
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                                                                                                                                                    RESULT 2
PCT-US92-06809-1
PCT-US92-06809-1, Application PC/TUS9206809
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15, Application US/08676242C Patent No. 6143719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 60:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: AMINO ACID
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 32; Conserv
32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT-US92-06809-1
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  Matches
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Gaps

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Indels

Length 352;

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; SEQ ID NO 12

; LENGTH: 352

; TYPE: PRT

; ORGANISM: Unknown

; FEATURE:

; CTHER INFORMATION: Description of Unknown Organism:Rat

US-08-737-045-12
                                                                                                                                                                                                              Query Match 30.7%; Score 49.5; DB 2; Best Local Similarity 35.7%; Pred. No. 25; Matches 10; Conservative 7; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                       1 TLTHTITKLNAENNATFYFKIDNVKKAR 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-832-535-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Dennis, James W.
TITLE OF INVENTION: COMPOSITIONS COMPRISING MODULATORS OF CYTOKINES OF THE TITLE OF INVENTION: TGFB SUPERFAMILY AND A METHOD OF TREATMENT WITH SUCH A TITLE OF INVENTION: COMPOSITION (AS AMENDED)
CURRENT APPLICATION NUMBER: US/08/737,045A
CURRENT FILING DATE: 1997-03-20
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                    Sequence 11, Application US/08483926A
Patent No. 5821227
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: MODULATORS OF CYTOKINES OF THE TGF BETA
TITLE OF INVENTION: SUPERFAMILY AND METHODS FOR ASSAYING FOR SAME
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 king Street West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                       CITY: Toronto
STATE: Ontario
CONTRY: Canada
ZIP: MRH 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,926A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 49.5; DE
; Pred. No. 25;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: KUCGYGYK, Linda M.
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELERAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 TVKTALAAFNAQNNGT-YFKLVEISRAQ 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TLTHTITKLNAENNATFYFKIDNVKKAR 28
Sequence 12, Application US/08737045A
Patent No. 5981483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 30.7%;
Best Local Similarity 35.7%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Rat
                                                                                                                   US-08-483-926A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-483-926A-11
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                                                                                                                                                                                                                                                                                             ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/83,535
FILING DATE: 03-APR-1997
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: KIMBALL, PAUL C.
REGISTRATION NUMBER: 9F265
FELECOMMUNICATION NUMBER: 9F265
TELECOMMUNICATION NUMBER: 14,610
REGISTRATION SOFT 1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 145 amino acids
TELENGT: 11near
                                                                                                                                                                                                         ADDRESSEE: HUMAN GENOME SCIENCES, INC. STREET: 9410 KEY WEST AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 HIITKLNAENNATFYFKIDNVKKARVQVV 32
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                                                                                                                                              HUMAN CYSTATIN
Sequence 2, Application US/08832535
Patent No. 5919658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
US-09-019-485-2
; Sequence 2, Application US/09019485
                                       GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: LI, HAODON
APPLICANT: YU, GUO-LIANG
APPLICANT: YU, GUO-LIANG
APPLICANT: GENTZ, REINER L
TITLE OF INVENTION: HUMAN CYS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 34.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-832-535-2
                                                                                                                                                                                                                         STREET: 9410 ALL
                                                                                                                                                                                                                                    CITY: KCC.
STATE: MD
COUNTRY: US
TP: 20850
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US-09-431-480-9
; Sequence 9, Application US/09431480
; Patent No. 6235708
; GENERAL INFORMATION:
; APPLICANT: HOLLOWAY, James L.
; APPLICANT: HOLLOWAY, James L.
; APPLICANT: Feldhaus, Andrew
; TITLE OF INVENTION: TESTIS SPECIFIC CYSTATIN-LIKE PROTEIN CYSTATIN T
FILE REFERENCE: 98-72
; CURRENT APPLICATION NUMBER: US/09/431,480
; CURRENT FILING DATE: 1999-11-01
; EARLIER APPLICATION NUMBER: 60/109,217
; EARLIER APPLICATION NUMBER: 60/156,382
; EARLIER APPLICATION NUMBER: 60/156,382
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Patent No. 644529

GENERAL INFORMATION:
APPLICANT: Holloway, James L.
APPLICANT: Feldhaus, Andrew
TITLE OF INVENTION: TESTIS SPECIFIC CYSTATIN-LIKE PROTEIN CYSTATIN T
FILE REFERENCE: 98-72 C1
CURRENT APPLICATION NUMBER: US/09/617,302

CURRENT FILING DATE: 2000-07-17
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15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13;
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Pred. No. 15;
6; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                            29.8%; Scor.
34.5%; Pred. No. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 HIITKLNAENNATFYFKIDNVKKARVQVV 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 HTITKLNAENNATFYFKIDNVKKARVQVV 32
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          APPLICATION NUMBER: US/09/019,485
                                                                                                                                 PF265P1
                                                          ATTORNEY AGENT INFORMATION:
NAME: Benson, Robert H.
REGISTRATION UNDBER: 30,446
REFERENCE/FOCKET MUMBER: 9F265
TELECAMUNICATION INFORMATION:
TELEFAX: 3013098439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 145 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29.8%;
34.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 29.8'
Best Local Similarity 34.5'
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-019-485-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens US-09-431-480-9
                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 10; Conserv
                                                 CLASSIFICATION:
                                FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-617-302-9
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                                                                                                                                                                                                                                                                                         ZIP: 20850
ZIP: 20850
MEDIUM TYPE: FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATR:
APPLICATION NUMBER: US/09/019,485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO COMPATIBLE
COMPOTER: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELease #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                      STREET: 9410 Key West Avenue CITY: Rockville STATE: MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 HIITKLNAENNATFYFKIDNVKKARVQVV 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF265P1
Patent No. 6066617

GENERAL INFORMATION:
APPLICANT: Li, Haodong
APPLICANT: Yu, Guo-Liang
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
TITE OF INVENTION: Cystatin F
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Li, Hacdong
APPLICANT: Yu, Guo-Liang
APPLICANT: Gentz, Reiner
APPLICANT: Ni, Jian
TITLE OF INVENTION: Cystatin F
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Benson, Robert H.
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PF26:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3013098504
TELEPHONE: 3013098439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09019485 Patent No. 6066617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 145 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein US-09-019-485-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
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Gaps
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19;
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          13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: PETERSEN, CAROLYN
APPLICANT: LEECH, JAMES
APPLICANT: NELSON, RICHARD, C.
APPLICANT: GUT, JIRI
TITLE OF INVENTION: POLYPEPTIDES BINDING ANTI-
                                                                                                                                                                                                                                              APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
TITLE OF INVENTION: NOVEL HUMAN CYSTATIN-LIKE
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/314,777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 48; DB Pred. No. 19; 6; Mismatches
          6; Mismatches
                                                                         PF-0193 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77 YSVEKFUNCTNDMFLFKESRITRALVQIV 105
                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals,
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                  4 HIITKLNAENNATFYFKIDNVKKARVQVV 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 HIITKLNAENNATFYFKIDNVKKARVQVV 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/791,522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-415-751-20
; Sequence 20, Application US/08415751
Patent No. 5643772
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTATION UNDRER: 36,749
REFERENCE/FOCKET NUMBER: PF-0:
RECCOMMUNICATION INFORMATION:
TELEFONE: 415-85-055
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                   US-09-314-777-1; Sequence 1, Application US/09314777; Sequence No. 6110686; Patent No. 6110884; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29.8%;
ilarity 34.5%;
Conservative
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 178 amino acid
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMMEDIATE SOURCE:
CLONE: 30443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94304
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          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08791522
| Patent No. 5995817
| GENERAL INFORMATION:
| APPLICANT: Bandman, Olga | APPLICANT: Bandman, Olga | APPLICANT: Goli, Surya K. | TITLE OF INVENTION: NOVEL HUMAN CYSTATIN-LIKE | TITLE OF INVENTION: NOVEL HUMAN CYSTATIN-LIKE | TITLE OF INVENTION: PROTEIN | NUMBER OF SEQUENCES: 4 | CORRESPONDECA ADDRESSE: Incyte Pharmaceuticals, Inc. | STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 48; DB 2;
Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,522
FILING DATE: Filed Herewith
PRIOR APPLICATION NUMBER: 09/431,480
PRIOR FILING DATE: 1999-11-01
PRIOR PLLICATION NUMBER: 60/109,217
PRIOR PILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: 60/156,382
PRIOR FILING DATE: 1999-09-28
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF-0193 US
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                                                                                                                                                                                                                                                                                                                                                                                                                    55 YSVEKFUNCTUDMFLFKESRITRALVOIV 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/POCKET NUMBER: PF-0
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-85-0555
TELEPAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 178 amino acids
TYPE: amino acid
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34.5%;
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Best Local Similarity 34.5'
Matches 10; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                            ORGANISM: Homo sapiens US-09-617-302-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                        LENGTH: 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-791-522-1
                                                                                                                                                                   SEQ ID NO 9
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Search completed: July 1, 2002, 16:18:02 Job time: 46 sec
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50.0%;
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MEDIUM TYPE: Floppy disk
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Best Local Similarity
Matches 9; Conserv
                     Texas
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                                               COUNTRY:
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Patent No. 6143559
GENERAL INFORMATION:
APPLICANT: Michael, Nancy M
APPLICANT: Accavitti, Marianne
APPLICANT: Thompson, Craig B
TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 48; DB 1; Length 350;
Pred. No. 40;
4; Mismatches 10; Indels
       CRYPTOSPORIDIUM ANTIBODIES, DNA AND RNA ENCODING THEM, HYBRID VECTOR AND TRANSFORMED HOST AND METHODS FOR IMMUNOTHERAPY AND DIAGNOSIS AND KIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Kb storage
COMPUTER: PC
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TITLE OF INVENTION: CRYPTOSPORIDIUM ANTIBODIES, I TITLE OF INVENTION: AND RNA ENCODING THEM, HYBRII TITLE OF INVENTION: DECTOR AND TRANSFORMED HOST ITLE OF INVENTION: METHODS FOR IMMUNTHERAPY AND TITLE OF INVENTION: DIAGNOSIS AND KIT NUMBER OF SEQUENCES: 50 CORRESPONDENCE ADDRESS: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       480.19-2 (HHD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/415,751
FILING DATE: 03-APR-1995
CLASSIPFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/071,880
FILING DATE: June 1, 1993
APPLICATION NUMBER: 07/891,301
FILING DATE: MAY 29, 1992
ATTORNEY AGENT INFORMATION:
NAME: Hana Dolezalova
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cryptosporidium parvum
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ilarity 39.1%;
Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity
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US-08-415-751-20
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Houston

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Pred. No. 24;
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,359
FILING DATE: CONCURRENTLY HERWITH
CLASSIFICATION: 510
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L
REGISTRATION NUMBER: 37,642
REJERDANCE/DOCKET NUMBER: ARSB:504
TELEPHONE: 512/448-3000
TELEPHONE: 512/448-3000
TELEPHONE: 512/448-7577
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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Human cystatin F.
Mature human cystatin F.
Human cystatin F.
Human cystatin F p.
Human cystatin F p.
Secreted protein C.
Mouse IMC carcinom
Human cystatin-lik
S. epidermidis ope
S. epidermidis ope
B. burgdorferi ant
Novel human secret
Novel human secret
Drosophila melanog
Mitochondrial EF-T
Anti-angiogenic D3
Anti-angiogenic D3
Peptide identified
Mouse IMC carcinom
                                                                         Drosophila melanog
Human mutant cysta
Human mutant cysta
                                                                                                                                                 Arabidopsis thalia
Arabidopsis thalia
Human kininogen D3
                                                                                                                                                                                      Amino acid sequenc
Amino acid sequenc
                                                                                                             Bovine mutant cyst
                                                                                                                          Human mutant cysta
Human mutant cysta
                                                  Anti-angiogenic
Anti-angiogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anti-angiogenic; anglogenesis; inhibitor; kininogen; homologue; endothelial cell proliferation; apoptosis; cancer; ocular disorder; rheumatoid arthritis; cytostatic; antiarthritic; antirheumatic; therapy; human; D3 peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                       AAB08553
AAW98907
AAY95406
AAY95407
ABB62195
AAY81200
                                                                                    AAY81200
AAY81189
AAY81218
AAY81198
AAY81198
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AAE04439
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                                                                                                                                                  AAG58
AAG58
AAB37
                                                                                                                                                                                                    AAB37
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  99WO-US28465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0112427.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anti-angiogenic D3 peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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WO200035407-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-DEC-1999;
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AAY95408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY95408
 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human high mol.wt.
Novel human diagno
Novel human diagno
Novel human diagno
Novel human diagno
Bradykinin protein
Bradykinin protein
Bradykinin analogo
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| SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
| SIDSI/gcgdata/hold-geneseqy-embl/AA1981.DAT:*
| SIDSI/gcgdata/hold-geneseqy-embl/AA1981.DAT:*
| SIDSI/gcgdata/hold-geneseqy-embl/AA1983.DAT:*
| SIDSI/gcgdata/hold-geneseqy-embl/AA1983.DAT:*
| SIDSI/gcgdata/hold-geneseqy-embl/AA1985.DAT:*
| SIDSI/gcgdata/hold-geneseqy-embl/AA1989.DAT:*
| SIDSI/gcgdata/hold-geneseqy-embl/AA1989.DAT:*
| SIDSI/gcgdata/hold-geneseqy-embl/AA1989.DAT:*
| SIDSI/gcgdata/hold-geneseqy-embl/AA1989.DAT:*
| SIDSI/gcgdata/hold-geneseqy-embl/AA1999.DAT:*
| SIDSI/gcgdata/hold-geneseqy-embl/AA1999.DAT:*
| SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
| SIDSI/gcgdata/hold-geneseqy-geneseqp-embl/AA1999.DAT:*
| SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
| SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
| SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
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Domaine 3, bradyki
Human kininogen D3
                                                                                   1, 2002, 16:19:44 ; Search time 95.97 Seconds
(without alignments)
37.036 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                                    747574
           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                             1 TLTHTITKLNAENNATFYFKIDNVKKARVQVV 32
                                                                                                                                                                                                                                                 hits satisfying chosen parameters:
                                                                                                                                                                                                                           747574 seqs, 111073796 residues
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                                                                                                                                                                                                                                                                                                                           Maximum Match 100%
Listing first 45 summaries
                                                              - protein search, using sw model
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AAY95426
ABG21101
ABG21099
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AAR33350
                                                                                                                                                                                                  Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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117
122
123
644
369
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                                                                                     July
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100.0
100.0
97.5
95.0
88.8
72.0
69.6
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Total number of

Searched:

Minimum DB Maximum DB

Database

Perfect score:

Sequence:

OM protein

: o

Run

Scoring table:

Composition for inhibiting angiogenesis and endothelial cell proliferation, inducing endothelial cell apoptosis and treating cancer,

WPI; 2000-442247/38.

ABG21102 ABG21105

161 161 161 161 161 161 153 173 116 116

10 10 10 110

Score

Result g AAP40633 AAP40257 AAW54336

18

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RESULT 3
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rheumatoid arthritis, and ocular disorders comprises a kininogen domain
                                                                                                                                                                                                                                                                                                                                                                                                                                  Domain 3; human; kininogen; heavy chain; low molecular weight; plasma; trypsin; platelet; activation; granule contents; hemostasis; thrombin; tissue plasminogen activator; thrombosis; inflammatory response; endothelial cell; von Willebrand factor;
                                                 The present sequence is that of a D3 peptide derived from human high mol.wt. kininogen (HK) domain 3 (see AAY95426). The D3 peptide inhibits endothelial cell proliferation and thus possesses anti-angiogenic activity. It is an example of D3 peptides of the invention (see AAY95405-26) that are analogues of certain sites in the HK domain 3, in this case amino acid residues Asn275-Lys283. The peptides inhibit endothelial cell proliferation and may also induce endothelial cell apoptosis. Compositions including the peptides are used in claimed methods for inhibiting anglogenesis, inhibiting endothelial cell proliferation, and inducing endothelial cell proliferation, and inducing endothelial cell proliferation, and inducing endothelial cell apoptosis. Cancer, rheumatchid arthritis, and ocular disorders characterized by undesired vascularization of the retina are treated.
                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                              Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Use of trypsin-cleavage fragment of human kininogen - for increasing vascular bradykinin release, for lowering blood pressure and treating hypertension
                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                            100.0%; Score 161; DB 21; 100.0%; Pred. No. 3.6e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                Domaine 3, bradykinin release activating peptide.
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                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                        1 TLTHTITKLNAENNATFYFKIDNVKKARVQVV 32
                                                                                                                                                                                                                                                                                  "Mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Leader peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                 AAR33350 standard; protein; 117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 1; 46pp; English.
                                Claim 4; Page 26; 44pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91US-0744545.
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                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UTEM ) UNIV TEMPLE.
                                                                                                                                                                                                                                       Similarity 32; Conserv
                                                                                                                                                                                               32 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9303748-A
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                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                               Query Match
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            3 analog
                                                                                                                                                                                                                                          Local
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Matches
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The sequence given represents domain 3, amino acids 246-362, of the human kiningen heavy chain. Domain 3 was isolated from low molecular weight kiningen, derived from human plasma, by cleavage with trypsin. Domain 3 peptide inhibits platelet activation causing a marked decrease in the platelets ability to aggregate and secrete their granule contents. The granule contents comprise proteins which participate in hemostasis, thrombosis and the inflammatory response. Domain 3 also inhibits endothelial cell activation shown by a decrease in secretion of endothelial cell contents such as tissue plasminogen activator and von Willebrand factor. Domain 3 functions to inhibit cell activation by blocking thrombin binding to its target cells, the peptide is a selective inhibitor of thrombin-induced platlet
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Pred. No. 1.7e-14;
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                            AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-APR-1999;
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Conservative

32;

Matches

25-SEP-2000 (first entry)

AAY95426;

AAY95426

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymeratase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The compinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in chagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and and can on orid sequences. ABGOOID-ABG30377 represent novel human cald sequences and for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the vipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful in of mutations
                                                                                                                                                                                                                                                                       Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
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100.0%; Pred. No. 1.2e-13;
iive 0; Mismatches 0;
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                                                                                                                                                                                                    Novel human diagnostic protein #21092.
   ABG21101 standard; Protein; 644 AA.
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ABG21099
ID ABG21099 standard; Protein; 369 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAR-2001; 2001WO-US08631
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2000US-0649167.
                                                                                                                                     (first entry)
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N-PSDB; AAS85288.
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                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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23-AUG-2000;
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                                                                                                                                     18-FEB-2002
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                                                                  ABG21101;
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   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        kiningen (HK). The invention provides peptides (see AAY95405-24) that are analogues of certain sites in the HK domain 3, specifically Aan275-Lys282, cys246-cys249, Leu331-Tyr338 and Tyr299-Ser314. The peptides, in which native cys residues may be replaced by Ala residues, inhibit endothelial cell proliferation and may also induce endothelial cell apoptosis. Compositions including the peptides are used in claimed methods for inhibiting anglogenesis, inhibiting endothelial cell proliferation, and inducting endothelial cell apoptosis. Cancer, rheumatoid arthritis, and ocular disorders characterized by undesired vascularization of
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100.0%; Pred. No. 1.7e-14;
ive 0; Mismatches 0;
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Mismatches
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                                                                                                  1 TLTHTITKLNAENNATFYFKIDNVKKARVQVV 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human high mol.wt. kininogen domain 3.
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99WO-US28465 98US-0112427

WO200035407-A2. Homo sapiens.

(UTEM ) UNIV TEMPLE. (MCCR/) MCCRAE R K.

16-DEC-1998; 02-DEC-1999; 22-JUN-2000.

WPI; 2000-442247/38

analog

The

McCrae RK;

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Gaps

32; Conservative

Matches

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RESULT ABG21101

53

Query Match Best Local Similarity

the retina are treated

Sequence 123 AA;

18-FEB-2002

ABG21099;

11-OCT-2001

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The inventor claims to isolated polymuciacule (1) and the inventor fracts: (1) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The and gene mapping, and in recombinant production of (II) the control of claims are also used in recombinant production of (II). The control or dentifying expressed genes. (1) is useful in gene therapy techniques for restore normal activity of (II) or to treat disease states involving (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in adaptostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and and no produce other types of data and products dependent on DNA and diagnostic amino acid sequences of the invention.

Sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                      Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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100.0%; Pred. No. 4.7e-13;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20; SEQ ID No 51461; 103pp; English.
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                                                                                                                                                Novel human diagnostic protein #21093.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                      18-FEB-2002 (first entry)
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Best Local Similarity 100.
Matches 30; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-639362/73.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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ABG21102:
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ABG21105
NOT COULD CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, common and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in disorders incombine for generations of the sequences. ABG00010-ABG30377 represent novel human and angone other trypes of data and products dependent on DNA and amino acid sequences of the invention.

Commino acid sequence data for this patent did not appear in the printed sequences the invention.

Note: The sequence data for this patent did not appear in the printed set fitp. Wipo. int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                     Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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100.0%; Pred. No. 2.1e-13;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 20; SEQ iD No 51458; 103pp; English.
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                                                                                                                                                                           Novel human diagnostic protein #21090
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23-AUG-2000; 2000US-0649167.
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Best Local Similarity 100.
Matches 31; Conservative
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N-PSDB; AAS85286.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200175067-A2.
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Gaps

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Length 248; Indels

Sequence

RESULT 7 7 ABG21102

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us-09-461-061a-4.open.rag

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Bradykinin is a peptide consisting of nine amino acids. It has the biological effect of decreasing blood pressure. Although kininogen is known as a protein-precursor of bradykinin, its structure is unknown because of the difficulty in collecting large enough samples of kininogen for structural investigation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          c-Dna fragment of protein precursor - used to code bradykinin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72.0%; Score 116; DB 5; Length 434; 74.2%; Pred. No. 1e-07; ive 3; Mismatches 5; Indels
                                                                                                                                                                                                                                 /note= "probe (AAN40241)-encoded sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     380..388
Jabol- bradykinin
393..397
/note= "probe (AAN40241)-encoded sequence"
                                              Bradykinin protein precursor: type II (pKG146, pKG254).
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                                                                                                                                      Location/Qualifiers 378..386 /label- bradykinin 391..395
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                                                                                            Blood pressure; kininogen; probe..
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(first entry)
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Best Local Similarity
Matches 23; Conserv
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30-JUL-1992
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                                                                                                              Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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Pred. No. 2.1e-11;
1; Mismatches 2;
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                                                                  Novel human diagnostic protein #21096
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23-AUG-2000; 2000US-0649167
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Matches 29; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                        Inhibition; thrombin-induced platelet; prevention; platelet aggregation; ADP-induced activation.
                                                                                           Bradykinin is a peptide consisting of nine amino acids. It has the biological effect of decreasing blood pressure. Although kininogen is known as a protein-precursor of bradykinin, its structure is unknown because of the difficulty in collecting large enough samples of kininogen for structural investigation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Administration of a peptide or multimer related to bradykinin or other disclosed peptides and multimers can be used for the inhibition of thrombin-induced platelets or other cells. They can also be used for preventing platelet aggregation, or inhibiting ADP-induced activation. This is useful to prevent arterial occlusions arising from coronary thrombosis and stroke.
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inhibition of platelet activation and aggregation - by admin. of
                                                                                                                                                                                                              ;
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                                                   c-Dna fragment of protein precursor - used to code bradykinin
                                                                                                                                                                                        Length 436;
                                                                                                                                                                                 69.6%; Score 112; DB 5; Length 43 71.0%; Pred. No. 3.6e-07; ive 4; Mismatches 5; Indels
                                                                                                                                                                                                                                             2 LTHTITKLNAENNATFYFKIDNVKKARVQVV 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 44; 73pp; English.
                                                                      Disclosure; Fig 2; 6 pp; Japanese.
                                                                                                                                                                                                                                                                                                        AAW54336 standard; peptide; 26 AA
                                                                                                                                                                                                                                                                                                                                                                       Bradykinin analogous peptide 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or known bradykinin analogues
(MITU ) MITSUBISHI CHEM IND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96WO-US09940.
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                                                                                                                                                                                       Query Match 69.6
Best Local Similarity 71.0
Matches 22; Conservative
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                  WPI; 1984-216122/35.
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                                                                                                                                                         436 AA;
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                             N-PSDB; AAN40242
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                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                          Sequence
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Length 26;

Score 95; DB 18; ] Pred. No. 2.9e-06;

59.0%; S 100.0%;

Query Match Best Local similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Composition for inhibiting angiogenesis and endothelial cell proliferation, inducing endothelial cell apoptosis and treating cancer, rheumatoid arthritis, and ocular disorders comprises a kininogen domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-angiogenic; angiogenesis; inhibitor; kininogen; homologue; endothelial cell proliferation; apoptosis; cancer; ocular disorder; rheumatoid arthritis; cytostatic; antiarthritic; antirheumatic;
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100.0%; Pred. No. 5.3e-05;
ive 0; Mismatches 0;
                                                                                                                                                                                                                      AAY95410 standard; Peptide; 16 AA.
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Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                               Anti-angiogenic D3 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       therapy; human; D3 peptide
                                                                                                                                                                                                                                                                                                                                                (first entry)
                                 13 NNATFYFKIDNVKKAR 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-442247/38.
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(MCCR/) MCCRAE R K.
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tes 16; Conserv
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AAY95409;

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RESULT

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The specification describes a method for identifying a peptide having a particular function. The method comprises preparing a database of polynucleotides and polypeptides of unknown functions, screening the database for a combination of nucleotides or amino acids indicative of the peptide with a particular function, and identifying polynucleotides and proteins which contain the peptide. The method is used to identify precursor peptides with an amidated C-terminus, especially polypeptide hormones, for studying physiologically active substances. The present sequence represents a peptide which was identified using the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying peptide with selected function, useful particularly for C-amidated hormones, by screening database for combination of nucleic acid and amino acid sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         carcinoma cell; IMC-HAl; cancer; metastasis; CMAP; inhibitor; metastasis associated protein.
                                                                                                  Precursor peptide; polypeptide hormone; peptide identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46.0%; Score 74; DB 21; Length 16
100.0%; Pred. No. 0.0012;
.ive 0; Mismatches 0; Indels
                                                           Peptide identified from an origin of prepro-bradykinine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Martinez J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SCRC ) SCRAS SOC CONSEILS RECH & APPL SCI (CNRS ) CNRS CENT NAT RECH SCI.
                                                                                                                                                                                                                          /note⇒ "hydrogen attached"
                                                                                                                                                                                                                                                                    /note= "amidated residue"
                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 16; Page 20; 40pp; French.
                                                                                                                                                                                                                                                                                                                                                                                               24-FEB-2000; 2000WO-FR00460.
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                   Key
Modified-site
                                                                                                                                                                                                                                              Modified-site
                                                                                                                                            Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is that of a D3 peptide derived from human high mol.wt. kininogen (HK) domain 3 (see AAY59426). The D3 peptide inhibits endothelial cell proliferation and thus possesses anti-anglogenic activity. It is an example of D3 peptides of the invention (see AAY59405-26) that are analogues of certain sites in the HK domain 3, in this case amino acid residues ABAD75-Lys282. The peptides inhibit endothelial cell proliferation and may also induce endothelial cell apoptosis. Compositions including the peptides are used in claimed methods for inhibiting anglogenesis, inhibiting endothelial cell proliferation, and inducing endothelial cell apoptosis. Cancer, rheumatoid arthritis, and ocular disorders characterized by undesired vascularization of the retina are treated. The ICSO value for the present peptide was less than 0.8 um for inhibition of fibroblast growth factor-induced HUVEC cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Composition for inhibiting angiogenesis and endothelial cell proliferation, inducing endothelial cell apoptosis and treating cancer, rheumatoid arthritis, and ocular disorders comprises a kininogen domain
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                                                                                                                                                                                                                      Anti-anglogenic; anglogenesis; inhibitor; kininogen; homologue; andthelial cell proliferation; apoptosis; cancer; ocular disorder; rheumatoid arthritis; cytostatic; antiarthritic; antirheumatic; therapy; human; D3 peptide.
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                                                        AAY95409 standard; Peptide; 16 AA.
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100.0%; Piv
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                                                                                                                                                                                 Anti-angiogenic D3 peptide
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Matches 16; Conser
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22-JUN-2000.

McCrae RK;

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Gaps

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Sequence

Query Match

õ g AAB08553

RESULT 14 AAB08553 ID AAB0855

Length 16;

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The present invention provides gene sequences associated with cancer metastasis which are isolated from mouse IMC carcinoma cells by detection of their higher expression in IMC-HM cell lines than in IMC-LM cell lines using differential display of the mRNA in these cells. The gene sequences can be used for the screening of potential inhibitors of cancer metastasis by either: bringing into contact with the cancer metastasis associated protein (CMAP) and determining the degree of binding; or creating a transformant cell line which expresses CMAP and measuring the degree of expression of CMAP using an antibody recognising the protein, either in the protein of CMAP using an antibody recognising inhibitor. IMC-HM cells transformed with antisense CMAP bNA show a lowered ability to metastasise. The present sequence represents a specifically claimed protein sequence from the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-JP01592.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-080732/07.
N-PSDB; AAX18513.
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Gaps

Search completed: July 1, 2002, 16:19:45 Job time: 149 sec

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APPLICANT: The Regents of the University of Michigan
APPLICANT: The Regents of the University of Michigan
APPLICANT: Schmaler, Alvin H.
APPLICANT: Hasan, Ahmed A.K.
TITLE OF INVENTION: Bradykinin Analogs As Selective Thrombin Inhibitors
FILE REFERENCE: 8820-2 US
CURRENT APPLICATION NUMBER: US/08/676,242C
CURRENT APPLICATION NUMBER: 60/000,096
EARLIER PILING DATE: 1995-06-09
EARLIER PILING DATE: 1995-06-09
EARLIER PILING DATE: 1996-06-07
NUMBER OF SEQ ID NOS: 24
SOFWMARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 26
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APPLICANT: Schmaler, Alvin H.
APPLICANT: Jiang, Yongping
TITLE OF INVENTION: Modulation of Blood
TITLE OF INVENTION: Pressure and Inhibition of Platelet Activation
TITLE OF INVENTION: with Kininogen Fragment
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seidel, Gonda, Lavorgna &
ý
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence: Bradykinin; OTHER INFORMATION: analog US-08-676-242-15
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                                                                                                                                                                                                                                                                                                                               Sequence
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Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 12; Conservative 0; Mismatches 0;
                              US-08-669-286-5
US-09-469-253-5
US-09-6421-46-5
US-09-621-855-2
US-09-621-855-2
US-08-453-2748-95
US-08-453-702A-95
US-08-453-702A-95
US-08-453-702A-95
US-08-453-702A-95
US-09-621-85-95
US-09-621-85-95
US-09-63-12588-95
PCT-US93-12588-95
US-09-621-95
US-08-453-702A-103
US-08-453-703A-103
US-08-453-703A-103
US-08-453-703A-103
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Sequence 15, Application US/08676242C
Patent No. 6143719
GENERAL INFORMATION:
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457
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US-08-193-114B-1
TYPE: PRT
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Sequence 9, Appli
Sequence 23, Appli
Sequence 74, Appl
Sequence 10, Appl
Sequence 51, Appli
Sequence 51, Appli
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Sequence 23, Appli
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Sequence 33, Appli
Sequence 33, Appli
Sequence 33, Appli
Sequence 33, Appli
Sequence 133, Appli
Sequence 133, Appli
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Sequence 1, Appli
Sequence 7, Appli
Sequence 5, Appli
Sequence 1, Appli
Sequence 174, Appli
Sequence 14, Appli
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                                                                                                                            July 1, 2002, 16:18:00 ; Search time 35.15 Seconds (without alignments) 8.339 Million cell updates/sec
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/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
                  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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PCT-08-193-114B-1
US-09-359-161-7
US-09-31-161-7
US-09-31-61-7
US-09-31-61-7
US-09-31-68-11
US-09-51-68-11
US-08-62-27A-14
US-08-62-27A-14
US-08-91-91-7
US-08-91-7
US-08-91-7
US-08-91-7
US-08-91-7
US-08-91-7
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US-08-91-7
US-08-144-925-23
US-08-144-925-23
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US-08-144-925-23
US-08-173-28-13
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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56
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Maximum DB seq length: 2000000000
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APPLICANT: Bradford, Kent J.
APPLICANT: Dahal, Peetambar
APPLICANT: Dahal, Peetambar
APPLICANT: Yang, Hong
APPLICANT: Downie, Bruce
APPLICANT: Gee, Oliver
APPLICANT: Gee, Oliver
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Regulation of Source-Sink Relationships and Responses
TITLE OF INVENTION: Conditions in Plants
FILE REFERENCE: 023070-095900US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: yeast sucrose nonfermenting protein kinase 1; OTHER INFORMATION: kinase subunit (SNF1) US-09-359-161-7
                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 56; DB 5; Length 117; 100.0%; Pred. No. 0.0014; Dive 0; Mismatches 0; Indels
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Sequence 5, Application US/08441139;
Patent No. 5773245;
GENERAL INFORMATION:
APPLICANT: Wittrup, Dr. Karl D.
APPLICANT: Robinson, Anne S.
TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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         744,545
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         APPLICATION NUMBER: Serial No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/09359161A Patent No. 6342656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
                             FILING DATE: 13 August 1991
ATTORNEY/AGENT INPORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
                                                                                                                      REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64.3%;
66.7%;
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: AMINO ACID
                                                                                                                                                                    TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 100.
Matches 12; Conservative
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PCT-US92-06809-1
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284 MDNIRKARV 292
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Sequence 1, Application PC/TUS9206809
GENERAL INFORMATION:
APPLICANT: Schmaler, Alvin H.
APPLICANT: Jiang, Yongping
TITLE OF INVENTION: Modulation of Blood
TITLE OF INVENTION: Pressure by Altering Bradykinin Levels
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Temple University - Of the
ADDRESSEE: Commonwealth System of Higher Education
STREET: Huilding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 56; DB 1; Length 117; Best Local Similarity 100.0%; Pred. No. 0.0014; Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Application
APPLICATION NUMBER: Serial No. 5472945 07/744,545
FILING DATE: 13 August 1991
ATTORNEY/AGENT INFORMATION:
                                                                                                             COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION UNDBER: US/08/193,114B
FILING DATE: 9 February 1994
CLASSIFICATION: 514
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOCTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06809
FILING DATE: 19910813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 30,480
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-137 CII
TELECOMMUNICATION INFORMATION:
TELEFAX: (215) 568-8383
TELEFAX: (215) 568-8383
TELEFEX: (215) 568-849
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Application
SSEE: Monaco, P.C.
F: 1800 Two Penn Center Plaza
Philadelphia
: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Philadelphia
STATE: Pennsylvania
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       ADDRESSEE:
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                                                                                              COUNTRY:
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Sequence 14, Application US/08622277A

Sequence 14, Application US/08622277A

Patent No. 6001580

GENERAL INFORMATION:
APPLICANT: Tani, Akiyoshi
APPLICANT: Ichimori, Yuzo
TITLE OF INVENTION: Method For Assaying MAP Kinase
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Funner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATA:
APPLICATION NUMBER: US/08/622,277A
FILING DATE: 27-MAR.1996
FILING DATE: 00-DEC-1995
PRIOR APPLICATION NUMBER: JP 320577-1995
FILING DATE: 24-NOV-1995
FILING DATE: 24-NOV-1995
                                                                                                                                                                                                                                                                                                                         Sequence 174 Application US/09188930A
Fatent No. 6150502
GENERAL INFORMATION:
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Steman, Matthew
APPLICANT: Offers Rene
APPLICANT: Offers Rene
APPLICANT: Offers Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FRASESQ for Windows Version 3.0
SEQ ID NO 174
LENGTH: 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.1%; Score 32; DB 4; Length 137; 75.0%; Pred. No. 50;
             85.7%; Pred. No. 1.5e+02;
ive 1; Mismatches 0;
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Best Local Similarity 75.0
Matches 6; Conservative
          Best Local Similarity 85.7
Matches 6; Conservative
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51 DKVKKARI 58
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178 IDNIKKA 184
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                                                                                                              1 IDNVKKA 7
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; ORGANISM: Human
US-09-188-930-174
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Sequence 1, Application US/09537682

Sequence 1, Application US/09537682

GENERAL INDOFMATION:
APPLICANT: TAKENCHI, Kenichi
APPLICANT: NAKANISHI, Yuji
APPLICANT: SUZUKI, Satoru
TITLE OF INVENTION: L-ALPHA-GIYCEROPHOSPHATE OXIDASE GENE,
TITLE OF INVENTION: L-ALPHA-GIYCEROPHOSPHATE OXIDASE GENE
TITLE OF INVENTION: L-ALPHA-GIYCEROPHOSPHATE
CURRENT APPLICATION NUMBER: US/09/537,682

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PALENTIN Ver. 2.1

SEQ ID NO 1

LENGTH: 607

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 34; DB 1; Lengtn v., Pred. No. 1.18+02;
TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS: ADDRESSE: SCULLY, SCOTT, MURPHY & PRESSER STREET: 400 Garden City Plaza CITY: Garden City
                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,139
FILING DATE: 15-MAY-1995
CLASSITICATION NUMBER: US 08/089,997
FILING DATE: 05-JUL-1993
ATTORNEY/AGENT IRPORMATION:
NAME: Didiglio, Frank S:
REGISTRATION NUMBER: 13,346
REFERENCE/DOCKET NUMBER: 8646
TELECOMMUNICATION INFORMATION:
TELEPRAX: S16-742-4366
TELERAX: S16-742-4366
TELERAX: S16-742-4366
TELERAX: S10-742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Enterococcus faecium No. 6303357 7044
US-09-537-682-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60.7%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 679 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 54.59
These 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :|| | |:||
476 VDNQKAVRIQV 486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino ac
STRANDEDNESS:
                                                                                                                                                                                                                                             USA
                                                                                                                                                                        CITY: Ga.
STATE: N
COUNTRY:
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g ò

TYPE: PRT

Query Match

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/product= "OTHER" /note= "amino acid 105 is glutamine, threonine or alanine"
                                                                                                                                                                                                                                                      /product= "OTHER" /note= "amino acid 106 is aspartic acid or histidine"
                                                                                                                                                                                                                                                                                                                                                           /product= "OTHER" /note= "amino acid 109 is glutamic acid or glycine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "OTHER" /note= "amino acid 110 is threonine or alanine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 360;
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60.0%; Pred. No. 1.4e+02;
tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR SIGNAL-RELATED KIRASE, SEQUENCES, AND METHODS OF PRODUCTION AND USE
                                         /note= "amino acid 103 is isoleucine or leucine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: SQUITE 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-206
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: MICTOSOFT WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,953A
FILING DATE: June 2, 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/029,494
FILING DATE: MAICH 19, 1993
ATTORNEY AGENT INCOMACIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/08459953A Patent No. 6030822 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lechner, Cornelia
APPLICANT: Moller, Niels P.H.
APPLICANT: Moller, Niels P.H.
TITLE OF INVENTION: EXTRACELLUL.
TITLE OF INVENTION: KINASE, SEQ
TITLE OF INVENTION: METHODS OF
TITLE OF INVENTION: AND USE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 57.1
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                       NAME/KEY: Region
LOCATION: 105..106
OTHER INFORMATION: /
                                                                                                                                                                                         FEATURE:
NAME/KEY: Region
LOCATION: 106.107
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                          LOCATION: 109..110
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: 110..111
; OTHER INFORMATION:
; OTHER INFORMATION:
US-09-025-580-2
                                            OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                    NAME/KEY: Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 DNVKKARVQV 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
US-08-459-953A-9
                      LOCATION:
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Patent No. 6162613

GENERAL INFORMATION:
APPLICANT: Su, Michael Shin-San
APPLICANT: Wilson, Reith Phillip
APPLICANT: Germann, Ursula A.
TITLE OF INVENTION: Methods For Designing Inhibitors of
TITLE OF INVENTION: Serine/Thereonine Kinases and Tyrosine Kinase
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 32; DB 3; Length 360;
Pred. No. 1.4e+02;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

COMPUTER: Floppy disk

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 070125-1995
FILING DATE: 28-MAR-1995
ATTORNEY, AGENT INFORMATION:
NAME: TOORbey, Kimberlin M.
REGISTRATION NUMBER: 35,391
REFERENCE/DOCKET NUMBER: 0421.0039-00000
TELECOMUNICATION INFORMATION:
TELEPHONE: (202)408-400
TELECOMUNICATION INFORMATION:
TELEPHONE: (202)408-400
INFORMATION FOR SED ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOMECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY ACENT INFORMATION:
NAME: Haley, James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: VPI 97-104
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.1%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 57.1
Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGLECULE TYPE: protein FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 DNVKKARVQV 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: US ZIP: 10020
                                                                                                                                                                                                                                                                                                                                                                                  US-08-622-277A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
US-09-025-580-2
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STATE:
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us-09-461-061a-3.open.rai

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lam, Joseph S.
APPLICANT: Burrows, Lori
APPLICANT: Charter, Deborah
APPLICANT: Charter, Deborah
APPLICANT: Charter, Deborah
TITLE OF INVENTION: No. 5994072el Proteins Involved in the Synthesis and Assembly
TITLE OF INVENTION: Of O-Antigen in Pseudomonas Aeruginosa
FILE REFERENCE: 6580-089
CURRENT APPLICATION NUMBER: US/08/846,762A
CURRENT FILING DATE: 1997-04-30
NUMBER OF SEQ ID NOS: 100
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 74
                                                                                                                                                                Sequence 233 Application US/0925292C

Patent No. 6245968
GENERAL INFORMATION:
APPLICANT: Boudec, Phillipe
APPLICANT: Boudec, Phillipe
APPLICANT: Boudec, Matthew
APPLICANT: Boudec, Matthew
APPLICANT: Bouns, Florence
TITLE OF INVENTION: Mutated hydroxyphenylpyruvate dioxygenase, DNA
TITLE OF INVENTION: Sequence and isolation of plants which contain such a
TITLE OF INVENTION: Gene and which are tolerant to herbicides
FILE REFERENCE: 5500*31
CURRENT APPLICATION NUMBER: US/09/252,292C
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1997-12-02
NUMBER OF SEQ ID NOS: 31
SEQ ID NO 23
LENGTH: 393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57.1%; Score 32; DB 2; Length 423; illarity 33.3%; Pred. No. 1.6e+02; Conservative 5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 74, Application US/08846762A; Patent No. 5994072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT; ORGANISM: Pseudomonas aeruginosa
US-08-846-762-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 57.1
Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Mus musculus US-09-252-292C-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 IDNVKKARVQVV 12
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Best Local Similarity
Matches 4; Conserva
                                                         :|:| |::||
300 ENLKSAKIQV 309
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301 ENLKSAKIQV 310
                                   2 DNVKKARVQV 11
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US-08-846-762-74
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                                                                                                                                                                                                                                                                                        Length 380;
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                                                                                                                                                                                                                                                                                      Score 32; DB 3; Length 380
Pred. No. 1.5e+02;
1; Mismatches 3; Indels
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Pred. No. 1.5e+02;
4; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: STUDNER, STEPHEN
APPLICANT: STURNER, STEPHEN
APPLICANT: SINGH, BLJAY
APPLICANT: BASCOMB, NEWELL
TITLE OF INVENTION: HPPD GENE AND INHIBITORS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAIDY & DAIDY PC
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: New York
STATE: NY
COUNTY: USA
ZID: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTESD for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,917A
FILING DATE: 25-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0646/1B917-US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/022,604
FILING DATE: 25-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: 21tron, Anne E.
REGISTRATION NUMBER: 41,391
REFERENCE/DOCKET NUMBER: 0646/1B6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08979917A
Patent No. 6118050
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEX: (213) 955-0440
TELEX: (57-3510
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 380 anino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 236687
INFORMATION FOR SEQ ID NO: 2:
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60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: No. 6118050e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 50.0%;
Matches 5; Conservative
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LENGTH: 392 amino acids
                                                                                                                                                                                                                                                                                      Query Match 57.1
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-459-953A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
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                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                                                        2 DNVKKARVQV 11
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                                                                                                                                                                               TOPOLOGY:
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US-08-979-917A-2
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US-08-750-717-2

| Sequence 2, Application US/08750717
| Sequence 2, Application US/08750717
| Patent No. 6180109
| GENERAL INFORMATION:
| APPLICANT: MOORMANN, Robertus J. M. APPLICANT: WONRANN, NUCLEOTION SET OF INVENTION: NUCLEOTION SET OF INVENTION: Trains, Polypeptides Encoded by These Sequences and Use:
| TITLE OF INVENTION: Infections of Pestivirus INVENTION: Infections NUMBER OF SEQUENCES: 11
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: YOUNG & THOMPSON STREET: YES ADDRESSEE: VOUNG & THOMPSON STREET: Virginia STATE: Virginia COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Pred. No. 3.5e+02;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER LOSA

ZIP: 2202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,717
FILING DATE: 24-DE-1996
CLASSIFICATION NUMBER: BP 94201743.5
PRIOR APPLICATION DATA:
APPLICATION NUMBER: BP 94201743.5
FILING DATE: 17-JUN-1994
PRIOR APPLICATION NUMBER: BP 94201743.5
ATTORNEY/AGBNT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32,925
REFERENCE/POCKET NUMBER: BO 39123
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 107-689-0573
TELEFX: 2488425 EMBON
                                                                       GENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Odell, Joan
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: Transcription Coactivators
FILE REFERENCE: BB-1165-9
CURRENT APPLICATION NUMBER: US/09/342,648
CURRENT FILING DATE: 1999-06-29
EARLIER FILING DATE: July 13, 1998
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Microsoft Office 97
SEQ ID NO 10
LENGTH: 890
                         Sequence 10, Application US/09342648 Patent No. 6248584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Ajellomyces capsulatus
US-09-342-648-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.1%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 57.1
Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :||:||:|
475 ENVQKAKIQ 483
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US-09-342-648-10
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; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CRARACTERSTICS:
; TYPE: amino acid
; TYPE: amino acid
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-750-717-2

Query Match
Best Local Similarity 75.0%; Pred. No. 1.6e+03;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps C

Qy 1 IDNVKAR 8
|||:|| |
|| Db 34.25 IDNLKKGR 34.32

Search completed: July 1, 2002, 16:18:01
Job time: 45 sec
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July 1, 2002, 16:20:38; Search time 46.58 Seconds (without alignments) 66.012 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                        OM protein - protein search, using sw model
                                                                                                                                                                 Run on:
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US-09-461-061A-4 161 1 TLTHTITKLNAENNATFYFKIDNVKKARVQVV 32 BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Sequence: Scoring table:

283138 seqs, 96089334 residues Searched:

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database :

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	kininogen, LMW pre	, HMW		, HMW	K-kininogen, LMW I	kininoqen, LMW I p		_	major acute phase	T-kininogen I prec	1	T-Kininogen, LMW I			ч	hypothetical prote		cysteine proteinas	probable lipoprote	site-specific reco	hypothetical coile	fetuin precursor -	probable disease r	hypothetical prote	aminopeptidase (le	hypothetical prote		hypothetical prote	
SUMMARIES	ID	KGHUL1	KGHUH1	KGBOL2	KGBOH2	A28055	KGBOL1	KGBOH1	A25486	KGRTM	KGRTT1	A23897	B28055	S49776	B97948	A44943	F90485	T33740	T10057	AH0548	A97177	T38834	A32827	G96610	E81356	G90558	AH1085	G90591	F82884	G70143
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	Query Match Length DB	427	644	434	619	433	436	621	639	423	430	430	430	498	217	701	803	139	209	364	523	306	375	709	313	459	768	1034	5005	377
ø	Query Match	100.0	100.0	72.0	72.0	9.69	9.69				60.9	6.09		32.6			32.0	31.7	31.7	31.7	31.7	31.1	30.7	30.7	30.4	30.4	30.4	30.4	30.4	29.8
	Score	161	191	116	116	112	112	112	112	66 .	98	98	86	52.5	52	52	51.5	51	51	51	51	20	49.5		49	49	49	49	49	48
	Result No.	п	7	٣	4	Ŋ	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

ORF MSV261 leucine	hypothetical prote	hypothetical prote	hypothetical prote	translation elonga	translation elonga	translation elonga	translation elonga	hypothetical prote	type III site-spec	DNA mismatch repai	topoisomerase iv s	cystatin - puff ad	cytidylate kinase	hypothetical prote	hypothetical prote
T28423	A86359	T21642	T24886	S50139	568466	S62768	S62767	G75105	803208	A97750	E90558	A28793	C82903	E71807	T29188
7	~	~	N	~	7	N	7	~	~	7	7	~	7	7	7
624	1231	107	107	392	452	452	452	454	645	890	939	111	224	256	431
29.8	29.8	29.5	29.5	29.5	29.5	29.5	29.2	29.5	29.5	29.5	29.5	29.5	29.5	29.5	29.5
48	48	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47	47	47	47
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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Riottspeich, F.; Kellermann, J.; Henschen, A.; Foertsch, B.; Muller-Esterl, W. Bur. J. Blochem. 152, 307-314, 1985
A;Title: The amino acid sequence of the light chain of human high-molecular-mass kini A;Reference number: A91153; MUID:86030270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Kellermann, J.; Lottspeich, F.; Henschen, A.; Mueller-Esterl, W. in Kinins IV, Greenbaum, L.M., and Margolius, H.S., ed., pp.85-89, Plenum Press, New A;Title: Amino acid sequence of the light chain of human high molecular mass kininoge
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A; Residues: 1-19;189-192;310-314;381-389 <LEN1>
B; Rsto, H.; Matsumura, Y.; Maeda, H.
F; Kato, H.; Matsumura, Y.; Maeda, H.
FEBS Lett. 232, 252-254, 1988
A; Title: Isolation and identification of hydroxyproline analogues of bradykinin in humber: A; Reference number: A61495; MUID:88211869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein
A; Moledues: 379-644 C.DOT>
A; Residues: 379-644 C.DOT>
A; Note: the bradyinin sequence preceding the light chain sequence was not determined A; Note: the bradyinin sequence preceding the light chain sequence was not determined R; Kellermann, J: Lottspeich, F.; Henschen, A.; Mueller-Esterl, W.
Eur. J. Blochem. 154, 471-478, 1986
Eur. J. Blochem. 154, 471-478, 1986
A; Title: Completion of the primary structure of human high-molecular-mass kininogen. A; Reference number: A24871; MUID:86108361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein
A; Mesidues: 380-389 <5x5>.
R; Lenarcic, B.; Gabrijelcic, D.; Rozman, B.; Drobnic-Kosorok, M.; Turk, V.
Biol. Chem. Hoppe-Seyler 369, 257-261, 1988
A; Title: Human cathepsin B and cysteine proteinase inhibitors (CPIs) in inflammatory
A; Reference number: $02482; MUID:89076517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A Molecule type: protein
A Residues: 380-389 CMIN-
B Residues: 380-389 CMIN-
J. Biol. Chem. 263, 16051-16054, 1988
A Fittle: Purification and identification of [hydroxyprolyl(3)]bradykinin in ascitic
A; Reference number: A31905; MUID:89034061
A; Reference number: A31905
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A;Residues: 381-389 cAME.
R; Sasaguri, M.; Ikeda, M.; Ideishi, M.; Arakawa, K.
Biochem. Biophys. Res. Commun. 150, 511-516, 1988
A;Tille: Identification of [hydroxyproline(3)]-lysyl-bradykinin released from human
A;Reference number: A34030; MUID:88106632
A;Reference number: A34030
                                            FEBS Lett. 321, 93-97, 1993
A;Title: Cloning, expression and characterization of human kininogen domain 3.
A;Reference number: S32422; MUID:93223854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein
A; Molecule type: protein
A; Mesiduce: 379-389, K', 390-407, Q', 409-644 <KELZ>
R; Mindroiu, T.; Carretero, O.A.; Proud, D.; Walz, D.; Scicli, A.G.
Biochem. Biophys. Res. Commun. 152, 519-526, 1988
A; Title: A new Kinin molety in human plasma kininogens.
A; Reference number: A27699; MUID:88209021
A; Accession: A27699
             R.; Assfalg-Machleidt,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Note: this peptide had Pro-383 modified to 4-hydroxyproline A;Accession: C61495
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                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 'ANSM',253-377 <AUE>
A;Note: differences are due to known cloning
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             D.; Mentele,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: A24871
A; Molecule type: protein
A; Residues: 'Z', 20-380 <KEL1>
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A; Accession: A27899
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A; Residues: 380-389 <KAT1>
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A; Residues: 381-389 < KAT2>
                                                                                                                                                                                  A; Accession: S32422
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                                                                                                                                                                                                                                    Kilters Extructural features of plasma kinins and kininogens.

Altile: Structural features of plasma kinins and kininogens.

A. Fed Proc. 27, 25-57, 1968

A. Filtle: Structural features of plasma kinins and kininogens.

A. Contents: annotation; bradykinin

C. Comment: The Law Kininogen precursor is produced from the same gene as the HWM form (s C. Comment: Kininogen is a cysteine proteinase inhibitor, takes part in initiation of the C. Comment: Enadykinin, released from kininogen by kallikrein, is a potent vasodilator, is dene: ODB: NM

C. Someoria.

A. Feder: ODB: NM

A. Cross-references: GDB: 125256; OMIM: 228960

A. Map postition: 3427-3427

A. Introns: 65/3: 102/3: 111/1; 188/3: 224/3: 253/1; 310/3; 346/3; 375/3; 401/3

C. Superfamily: kininogen; cystatin homology of cysteine proteinase inhibitor; glyc C: Superfamily: kininogen; cystatin homology of cystain predicted cysta.

C. Superfamily: Marchinogen (Kininogen II) #status predicted cysta.

F. 19-18/Domain: signal sequence #status predicted cysta.

F. 19-18/Domain: systatin homology cxc1>
F. 19-18/Domain: cystatin homology cxc1>
F
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    T.; Nakanishi,
R;Kitamura, N.; Kitagawa, H.; Fukushima, D.; Takagaki, Y.; Miyata, T.; Nakanishi, J. Biol. Chem. 260, 8610-8617, 1985
A;Title: Structural organization of the human kininogen gene and a model for its A;Reference number: A92545; MUID:85234583
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A;Residues: 1-592,'I',594-644 <TAK>
A;Cross-references: GB:M11437; NID:g186751; PIDN:AAB59550.1; PID:g386852
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                                                                                                                                               A;Contents: annotation; gene organization R;Plerce, J.V.
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Matches 23; Conserv
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A.Title: Structural features of plasma kinins and kininogens.
A.Reference number: A91455; MUID:90255622
A.Contents: annotation; bradykinin
A.Contents: annotation; bradykinin
C.Comment: The HWW kininogen procursor and the LMW form are produced from the same gene C.Comment: Kininogen is a cysteine proteinase inhibitor, takes part in initiation of the C.Comment: The glycine/histidine/lysine-rich region of HWW kininogen light chain is import comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator, i xyproline residue is present in the kininogen prior to the release of bradykinin.
                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: protein
A;Residues: 264-359, NV. 361-375 <LEN2>
A;Residues: 254-359, NV. 361-375 <LEN2>
Biochem. J. 307, 341-346, 1995
A;Title: Human mast cell tryptase isoforms: separation and examination of substrate-spec A;Reference number: S55239; MUID:95251593
A;Accession: S55239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: protein
A;Residues: 450-452, X',454,'X',456 <LIT>
R;Straczek, J; Maachi, F; le Nguyen, D.; Becchi, M.; Heulin, M.H.; Nabet, P.; Bellevil
FEBS Lett. 373, 207-211, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Artitle: Purification from human plasma of a tetrapeptide that potentiates insulin-like A:Reference number: $68059; MUID:96033974
A:Reference number: $68059; MUID:96033974
A:Accession: $68059
A:Accession: $68059
A:Residues: 431-434 <5TR>
A:Residues: 431-434 <5TR>
B:Kitamura, N: Kitagawa, H: Fukushima, D.; Takagaki, Y.; Miyata, T.; Nakanishi, S.
J. Biol. Chem. 260, 8610-8617, 1985
A:Title: Structural organization of the human kininogen gene and a model for its evolutian a:Reference number: A92545; MUID:85234583
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A. Introns: 65/3; 131/1; 188/3; 224/3; 253/1; 310/3; 346/3; 375/3

A. Introns: 65/3; 131/1; 188/3; 224/3; 253/1; 310/3; 346/3; 375/3

C. Superfamily: kininogen; cystatin homology cody cystatin by the spirit of the
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F:19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) *status experimen
F:28-614.83-94,107-126,142-145,206-218,229-248,264-267,328-340,351-370/Disulfide bonds:
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F.169,205,294/Binding site: carbohydrate (Asn) (covalent) #status experimental
F.379-380/Cleavage site: Met-Lyg (kallikrein) #status experimental
F.389-380/Cleavage site: Arg-Ser (kallikrein) #status experimental
F.389-390/Cleavage site: Arg-Ser (kallikrein) #status experimental
F.401,533,542,546,557,571,593,628/Binding site: carbohydrate (Thr) (covalent) #status
F.577/Binding site: carbohydrate (Ser) (covalent) #status
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F;264-375/Domain: cystatin homology <CY3>
F;264-375/Domain: cystatin homology <CY3>
F;380-389/Product: lysyl-bradykinin (kallidin II) #status experimental <KBDY>
F;381-389/Product: bradykinin (kallidin I) #status experimental <BDY>
F;380-644/Domain: HWW kininogen light chain #status experimental <LCH>
F;421-510/Region: glycine/histidine/lysine-rich 30-residue repeats
                                                                                                                                                                                                                                                Ö.
                                             A;Residues: 380-389 <KAT3>
R;Lenarcic, B.; Krasovec, M.; Ritonja, A.; Olafsson, I.; Turk, V.
FEBS Lett. 280, 211-215, 1991
A;Title: Inactivation of human cystatin C and kininogen by human cathepsin A;Reference number: S14303; MUID:91192133
A;Reference: S14447
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Best Local Similarity
Matches 32; Conserv
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N; Concains: pragrayAnian (Asilian); Anianogen 1; Kininogen 11; prokinianogen (C.) Species: Boss primigenius taurus (catile)
C.) Cate: 14-Nov-1893 #sequence_revision 14-Nov-1983 #text_change 28-May-1999
C.A.Ccession: A01284
R; Nawa, H.; Kitamura, N.; Hirose, T.; Asai, M.; Inayama, S.; Nakanishi, S.
Proc. Nati. Acad. Sci. U. S.A. 80, 90-94, 1983
A.Title: Primary structures of bovine liver low molecular weight kininogen precursors A.R.Ccession: A01284
A; Molecule type: mRNA
A; Reference number: A93984; MUID: 83117859
A.A.Ccession: A01284
A; Molecule type: mRNA
A; Residerences: GB: V00427; GB: J00011; NID: 9489; PIDN: CAA23710.1; PID: 9490
C.; Comment: The LWM kininogen proteinase inhibitor, takes part in initiation of C; Comment: Rininogen is a cysteine proteinase inhibitor, takes part in initiation of C; Comment: Rininogen is a cysteine proteinase inhibitor, takes part in initiation of C; Comment: Rininogen is a cysteine proteinase inhibitor, cysteine proteinase inhibitor; cysteine proteinase inhibitor; cystein homology comparison; cystein homol
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Natternate names: alpha-2-thiol proteinase inhibitor; preprokininogen
N.Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen
N;Contains: bradykinin (kallidin); kininogen I; kininogen II; prokininogen
C;Species: Bos primigenius taurus (cattle)
C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 22-Jun-1999
C;Accession: A01282; A91941; A91938; B29559
C;Accession: A01282; A91941; A91938; B29559
C;Accession: N; Takagaki, Y; Furuto, S; Tanaka, T; Nawa, H; Nakanishi, S.
Nature 305, 545-549, 1983
A;Title: A single gene for bovine high molecular weight and low molecular weight kini
A;Accession: A0132
A;Accession: A0182
A;Accession: A0182
A;Accession: A0180
A;Residues: 1-619 <RTT
A;Residues: 1-619 <RTT
A;Residues: 1-619 <RTT
A;Accession: A0180
A;Residues: 1-619 <RTT
A;Accession: A0180
A;Accession: A01
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C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 28-May-1999
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Pred. No. 7.1e-08;
Mismatches 5; Indels
312
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J. Biochem. 67, 313-323, 1970
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Gaps

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for bradykinin

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kininogen, LAW I precursor - bovine
N;Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen
N;Contains: bradykinin (kallidin); kininogen I; kininogen II; prokininogen
C;Species: Bos primigenius taurus (cattle)
C;Species: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 22-Jun-1999
                                                                                                                                                            C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Jun-1989 #sequence_revision 20-Jun-1989 #text_change 15-Nov-1996
                                                                                                                                                                                                                                                                                                    R;Furuto-Kato, S.; Matsumoto, A.; Kitamura, N.; Nakanishi, S.
J. Biol. Chem. 260, 12054-12059, 1985
A;Title: Primary structures of the mRNAs encoding the rat precursors
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Pred. No. 2.4e-07;
2; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         282 LGHSIAQLNAENNHTFYFKIDTVKKATSQVV 312
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                                                                                                             K-kininogen, LMW I precursor - rat
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A;Residues: 1-433 <FURS.
C;Superfamily: kininogen; cystati
C;Keywords: alternative splicing
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Best Local Similarity
Matches 23; Conserv
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A; Residues: 1-436 <NAW>
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A. Residence of the light chain of human high-molecular-mass kininog and in the accession of the light chain of human high-molecular-mass kininog and the common of the accession of the light chain of human high-molecular-mass kininog and accession and the accession of the light chain of human high-molecular-mass kininog and accession and the accession of the a
                                                                                                                                                                                      A Accession: A91941

A Molecule type: protein

A J 1975

A J 1975

A Title: Studies on the primary structure of bovine high-molecular-weight kininogen. Ami

A Accession: A91938

A Accession: A91938

A MUD: 75170265

A Molecule type: protein

A Molecule type: Multiple type: metaly

A Molecule type: protein

A Molecule type: protein

A Molecule type: Multiple type: metaly

A Molecule type: protein

A Molecu
R;Han, Y.N.; Kato, H.; Iwanaga, S.; Suzuki, T.
J. Biochem. 79, 1201-1212, 1976
A;Title: Primary structure of bovine plasma high-molecular-weight kininogen. The amino
A;Reference number: A91941; MUID:76260155
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Pred. No. 1e-07;
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74.2%;
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Best Local Similarity
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A/Cross-references: GB:J00010; GB:V000426; NID:g163256; PIDN:AAA30604.1; PID:g163257
C;Comment: The LMW kininogen precursor is produced from the same gene as the HMW form
C;Comment: Bradykinin is a cysteine proteinase inhibitor, takes part in initiation of
C;Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator
xyproline residue is present in the kininogen prior to the release of bradykinin.
C;Superfamily: kininogen; cystatin homology
C;Superfamily: kininogen; cystatin homology
E;1-18/Domain: signal sequence #status predicted <AIG>
F;19-436/Product: LMW kininogen I #status predicted <AIG>
F;19-378/Product: LMW kininogen I heavy chain #status predicted
F;19-130/Domain: cystatin homology <CVI>
F;263-374/Domain: cystatin homology <CVI
F;263-374/Domain: cystatin
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R;Nawa, H.; Kitamura, N.; Hirose, T.; Asai, M.; Inayama, S.; Nakanishi, S.
Proc. Natl. Acad. Sci. U.S.A. 80, 90-94, 1983
A;Title: Primary structures of bovine liver low molecular weight kininogen precursors
A;Reference number: A93984; MUID:83117859
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Gaps

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5; Indels

3; Mismatches

23; Conservative

Matches

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2 LTHTITKLNAENNATFYFKIDNVKKARVOVV 32

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Accession: A25406

B;Kitagawa, H.; Kitamura, N.; Hayashida, H.; Miyata, T.; Nakanishi, S.
1. Biol. Chem. 262, 1907-1919

B;Kitagawa, H.; Kitamura, N.; Hayashida, H.; Miyata, T.; Nakanishi, S.
1. Biol. Chem. 262, 1907-2198

A;Title: Differing expression patterns and evolution of the rat kininogen gene family A;Reference number: A92625; MUID:87137443

A;Reference number: A92625; MUID:87137443

A;Reference number: A92625; MUID:87137443

A;Residue: 1639 KIIP-
A;Nolecule type: mRNA
A;Residues: 1-639 KIIP-
A;Note: the authors translated the codon CAA for residue 347 as Asn
C;Superfamily: kininogen, cystatin homology
C;Keywords: alternative splicing
F;1-18/Domain: cystatin homology ccx1>
F;19-131/Domain: cystatin homology ccx2>
F;264-375/Domain: cystatin homology ccx3>
                                                                                                                       Fig. Modified site: pyrolidone carboxylic acid (Gln) (in mature form) #status experiming the difference of pyrolidone carboxylic acid (Gln) (in mature form) #status experimental Fig. Modified site: pyrolidone carboxylic acid (Gln) (covalent) #status experimental Fig. 7-591, 82-93.106-125, 141-144, 205-217, 228-247, 263-266, 327-339, 350-369/Disulfide bond Fig. 7-107, 160-169, 204/Finding site: carbohydrate (Thr) (covalent) (partial) #status experimental Fig. 797/Finding site: carbohydrate (Asn) (covalent) (partial) #status experimental Fig. 797-379/Cleavage site: Met. 4-hydroxyproline (Fro) #status predicted Fig. 382/Modified site: A-hydroxyproline (Fro) #status experimental Fig. 382/Fid. Site: A-hydroxyproline (Fro) #status experimental Fig. 383-7406, 512, Fid. Midroxyproline (Fro) #status experimental Fig. 399, 400, 520, 524, 536, 548, 553, 570/Fid. site: carbohydrate (Ser) (covalent) #status Fig. 999/Cleavage site: Arg-Thr (kallikrein) #status experimental
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N;Contains: bradykinin
N;Contains: bradykinin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 12-Apr-1996
C;Accession: A01285
R;Cole, T; Inglis, A.S.; Roxburgh, C.M.; Howlett, G.J.; Schreiber, G.
R;Cole, T; Inglis, A.S.; Roxburgh, C.M.; Howlett, G.J.; Schreiber, G.
A;Title: Major acute phase alpha1-protein of the rat is homologous to bovine kininoge A;Reference number: A01285; MUID:85127561
A;Reference number: A01285
A;Rocession: A01285
A;Roce
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Kininogen, HWW I precursor - rat
N;Contains: bradykinin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 08-Mar_1989 #sequence_revision 08-Mar-1989 #text_change 15-Nov-1996
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Pred. No. 3.5e-07;
4; Mismatches 5;
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                                                                             F;417-488/Region: glycine/histidine/lysine-rich
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ilarity 71.0%;
Conservative
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Matches 22; Conserv
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Best Local Similarity
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A; Molecule type: protein
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C; Comment: The HWW kininogen precursor is produced from the same gene as the LMW form as
C; Comment: Kininogen is a cystelne proteinase inhibitor, takes part in intiatiation of the
C; Comment: The glycine/histidine/lysine-rich region of HWW kininogen light chain is impo
C; Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator, is a potent vasodilator.
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A; Cross-references: GB:V01491; GB:K01757; NID:g491; PIDN:CAA24735.1; PID:g492
A; Cross-references: GB:V01491; GB:K01757; NID:g491; PIDN:CAA24735.1; PID:g492
B; Kato, H.; Nagasawa, S.; Suzuki, T.
J. Biochem. 67, 313-323, 1970
A; Title: Studies on the structure of bovine kininogen: cleavages of disulfide bonds and A; Reference number: A91923; MUID:70180420
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A;Molecule type: protein
A;Residues: 378-393 «KAT»
R;Han, Y.N.; Komiya, M.; Iwanaga, S.; Suzuki, T.
B;Han, Y.N.; 55-68, 1975
A;Title: Studies on the primary structure of bovine high-molecular-weight kininogen. Ami
A;Reference number: A91938; MUID:75170265
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C; Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; dupl
F; 1-8 HOpomain: signal sequence #status predicted <SIG>
F; 19-621/Product: HWW prokininogen I #status predicted <MAT>
F; 19-379/Product: HWW kininogen I heavy chain #status experimental <HCH>
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F:263-347/Domain: cystatin homology <CY3>
F:379-388/Product: lysyl-bradykinin (kallidin II) #status experimental <KBDY>
F:380-388/Product: bradykinin (kallidin II) #status experimental <BDY>
F:389-621/Product: HMW kininogen I light chain #status experimental <LCH>
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A; Molecule type: protein
A; Residues: 458-498 < 4HAN>
B; Sueyoshi, T.; Miyata, T.; Hashimoto, N.; Kato, H.; Hayashida, H.; Miyata
J. Biol. Chem. 262, 2768-2779, 1987
A; Title: Bovine high molecular weight kininogen. The amino acid sequence,
A; Reference number: A92627; MUID:87137530
                                                                                                                                                                                                                   Gaps
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                                                                      Length 436;
Score 112; DB 1; Ler
Pred. No. 2.5e-07;
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                                                                      69.6%;
71.0%;
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Best Local Similarity
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A;Residues: 1-48 <KAG>
A;Cross-references: GB:M14356; NID:g205090;
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64.5%;
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A; Residues: 1-14 <AND1>
A; Accession: B23897
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A; Residues: 5~430 <AND2>
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A Ancession: A01286
A Ancession: D2548
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C; Keywords: bradykinin; cysteine proteinase inhibitor; duplication; glycoprotein; inflam F;1-11/Domain: signal sequence (fragment) #status predicted <SIG> F;1-14/Domain: signal sequence (fragment) #status predicted <SIG> F;12-423/Product: major acute phase alpha-1 protein #status predicted <WAT> F;12-123/Domain: cystatin homology <CY1> F;134-245/Domain: cystatin homology <CY2> F;256-65/Domain: cystatin homology <CY2> F;371-379/Product: bradykinin #status predicted <BDY> F;371-379/Product: bradykinin #status predicted acid (Gln) (in mature form) #status predicted F;161,197/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C:Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 22-Jun-1999
C;Accession: A01286; D25486; A28526; PL0193; J00027; B25488; A28525; S68036
R;Furuto-Kato, S.; Matsumoto, A.; Kitamura, N.; Nakanishi, S.
J Biol. Chem. 260, 12054-12059, 1985
A.Title: Primary structures of the mRNAs encoding the rat precursors for bradykinin and nhibitor.
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Pred. No. 1.3e-05;
4; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      274 LGHSIARLNAQHNHIFYFKIDTVKKATSQVV 304
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Best Local Similarity 64.5%;
Matches 20; Conservative
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R;Enjyoji, K.; Kato, H.; Hayashi, I.; Oh-ishi, S.; Iwanaga, S. J. Biol. Chem. 263, 965-972, 1988
A;Title: Purification and characterization of two kinds of low molecular weight kinin A;Reference number: A28525; MUID:88087225
A;Accession: A28525
                                                                                                                                                                                                                                                                                               A Residuce: 170 Carbon Malerian A Residuce: 376-430 Carbon Malerian A Residuce: 376-430 Carbon Malerian Fr.; Walter, R.; Vautravers, P.; Guigoz, Y. Arch. Blochem. Blophys. 322, 333-338, 1995
A; Tille: Identification of several isoforms of T-kininogen expressed in the liver of A; Reference number: 568034; MUID: 96032652
A; Reference number: 568036
A; Residuce: 340-430 CsIE>
A; Residuce: 340-430 CsIE>
A; Experimental source: clone pSG17
C; Comment: At least three types of LWM kininogen precursors are present in rat plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ceding bradykinin.
C;Comment: T-kininogens contain T-kinin (I-S-bradykinin), a novel kinin isolated afte d of an Arg or Lys, it is probably not released from its precursor by either tissue o C;Comment: The T-kininogens are produced in response to an inflammatory stimulant. C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aintrons: 65/3; 102/3; 130/1; 187/3; 223/2; 252/1; 309/3; 345/3; 374/3; 398/3
C; Superfamily: kininogen; cystatin homology
C; Superfamily: kininogen; cystatin homology
C; Superdial sequence #status predicted cSiG>
F; 19-430/Porduct: T-kininogen I #status experimental cMAT>
F; 19-130/Domain: systatin homology cCYI>
F; 19-130/Domain: cystatin homology cCYI>
F; 220/Domain: cystatin homology cCYI>
F; 241-252/Domain: cystatin homology cCYI>
F; 263-374/Domain: cystatin homology cCYI
F; 264-274/Domain: cystatin homology cYI
F; 264-274/Domain: cystatin homology cyicle cystatin homology cYI
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A)Note: the authors translated the codon CTC for residue 410 as Arg, CTA for residue C;Superfamily: Kininogen; cystatin homology
F;19-130/Domain: cystatin homology CCI>>
F;141.252/Domain: cystatin homology CCY>>
F;263-374/Domain: cystatin homology CCY>>
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Sacession: A23897; B23897
R;Anderson, K.P.; Heath, E.C.
J. Biol. Chem. 260, 12065-12071, 1985
A;Fitle: The relationship between rat major acute phase protein and the kininogens.
A;Reference number: A23897; MUID:86008266
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PIDN: AAA41492.1;
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Pred. No. 1.8e-05;
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Pred. No. 1.8e-05;
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1 Similarity 64.5%;
20; Conservative 4
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C;Species: Ieishmania mexicana amazonensis
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Aug-1999
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Aug-1999
C;Accession: A44444
A;Petaraz, G.
Mol. Blochem. Parasitol. 42, 247-256, 1990
A;Title: Sequence analysis and transcriptional activation of heat shock protein 83 of A;Title: Sequence number: A44443
A;Reference number: A44443
A;Status: preliminary
A;Mocession: A44443
A;Status: preliminary
A;Residues: 1-701 <SHA>
A;Coss-references: GB:M92926; GB:M34292; NID:g159351; PIDN:AAA29250.1; PID:g159354
C;Superfamily: heat shock protein 90
A; Accession: S51167
A; Molecule type: DNA
A; Residues: 231-498 < MUW>
A; Cross-references: EMBL:246727; NID:91289283; PID:e223644; PID:91289296; GSPDB:GN000
A; Note: the reading frame starts at the first ATG codon
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C. Species: Streptococcus pneumoniae
C. Date: 22-oct-2001 #sequence_revision 22-oct-2001 #text_change 22-oct-2001
C. Accession: B9748
C. Date: 22-oct-2001 #sequence_revision 22-oct-2001
C. Accession: B9748
C. D. J. J. Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.;
E. Hoskins, J. A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.;
Y. P.; Sun, P.M.; Winkler, M.E.
J. Batceriol. 183, 5709-5717, 2001
J. Batceriol. 183, 5709-5717, 2001
A.Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, B.; Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A.Reference number: A97872; MUD:21429245; PMID:11544234
A.Rocession: B9748
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A.Rocession: B9748
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Pred. No. 25;
5; Mismatches
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Pred. No.
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Best Local Similarity 41.4%;
Matches 12; Conservative
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45.5%;
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Matches 10; Conservative
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A;Gene: MIPS:YDR179w-a
A;Map position: 4R
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N;Alternate names: hypothetical protein YD9395.13
C;Species: Saccharomyces cerevisiae
C;Date: 13-Jan-1995 #sequence_revision 10-Feb-1995 #text_change 29-Oct-1999
C;Accession: 349776; S51167
R;Murphy, L.; Harris, D.E.
Submitted to the EMBL Data Library, November 1994
A;Reference number: S49776
A;Molecule type: DNA
A;Residues: 1-498 cMUR>
A;Residues: 1-498 cMUR>
A;Residues: 1-498 cMUR>
A;Cross-references: EMBL:246727; NID:91289283; PIDN:CAA86685.1; PID:e223726; PID:9128928
A;Note: the sequence extends from the previous stop codon and does not begin with a star
                                                                                                                                                                                                                                                                         T-kininogen, LMW II precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Jun-1989 #sequence_revision 20-Jun-1989 #text_change 12-Dec-1997
C;Accession: B28055; E25486; B28526; C28526
R;Furuto-Kato, S.; Matsumoto, A.; Kitamura, N.; Nakanishi, S.
J. Biol. Chem. 260, 12054-12059, 1985
A;Title: Primary structures of the mRNAs encoding the rat precursors for bradykinin and
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A:Residues: 375-430 «KTT>
A:Residues: 375-430 «KTT>
J. Biol., K.; Kato, H.; Hayashi, I.; Oh-ishi, S.; Iwanaga, S.
J. Biol. Chem. 263, 973-979, 1988
A:Title: Purification and characterization of rat T-kininogens isolated from plasma of
A:Reference number: A92729; MUID:88087226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1.430 < PUR>
R; Kitagawa, H.; Kitamura, N.; Hayashida, H.; Miyata, T.; Nakanishi, S.
J; Biol. Chem. 262, 2190-2198, 1987
A; Title: Differing expression patterns and evolution of the rat kininogen gene family.
A; Reference number: A92625; MUID: 87137443
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A;Residues: 'E',20-48;376-388,'R',390-419,'ER',422-430 <EN2>
C;Superfamily: Kininogen: cystatin homology
C;Keywords: glycoprotein: pyroglutamic acid
F;1-18/Domain: signal sequence #status predicted <SIG>F;19-430/Product: T-kininogen, LMW II #status experimental <MAT>F;19-130/Domain: cystatin homology <CVI>C;
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Pred. No. 1.8e-05;
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A; Residues: 'E', 20-25, 'MD', 28-48,376-430 <ENJ>
A; Accession: C28526
                                                                             281 LGHSIAQLNAQHNHLFYFKIDTVKKATSQVV 311
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                                 2 LTHTITKLNAENNATFYFKIDNVKKARVQVV
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64.5%;
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"Isolation of a human cDNA for alpha 2-thiol proteinase inhibitor and
its identity with low molecular weight kininogen.";
Biochemistry 23:5691-5697(1984).
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"Cloning and sequence analysis of cDNAs for human high molecular weight and low molecular weight prekininogens.";
two human prekininogens.";
J. Biol. Chem. 260:8601-8609(1985).
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                                                                                                                                                                                                                                                                           KNG_HUMAN STANDARD; PRT; 644 AA.
P01042; P01043;
21-UUL-1986 (Rel. 01, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Kininogen precursor (Alpha-2-thiol proteinase inhibitor) (Contains: Bradykinin)
           mink
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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        P27438 | P12929 | P43479 | P04945 | P04945 | P01034 | P01171 | P014171 | P57456 | P029544 | P59548 | P54682 | P
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Lottspeich F., Kellermann J., Henschen A., Foertsch B.,
Mueller-Esterl W.;
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                                                                                                                                                                                                         ALIGNMENTS
                                                KV6K_MOUSE
CYTC_BOVIN
CYTM_HUMAN
YE54_SCHPO
TRUB_BUCAI
                                                                                                                     EFT3_STRRA
EFTU_RECAM
GLNA_METMP
D7_DICDI
          VNCS_MEVA
VNCS_PAVCN
CGKB_ALTCA
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Copyright (c) 1993 - 2000 Compugen Ltd.
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KNL2_BOVIN
KNL1_BOVIN
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KNG_RAT
KNT1_RAT
KNT2_RAT
KNT2_RAT
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T2H2_HAEPA
CYTF_HUMAN
EFT3_STRCO
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T3MO_ECOLI
CYT_BITAR
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A2HS_MOUSE
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length: 2000000000
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HWW-KININOGEN PLAYS AN IMPORTANT ROLE IN BLOOD COAGULATION BY
HELPING TO POSITION OF PRIMALLY PREKALLIKREIN AND FACTOR XI NEXT TO
HELPING TO POSITION OF PRIMALLY PREKALLIKREIN AND FACTOR XI NEXT TO
FACTOR XII: (3) HWW-KININOGEN INHIBITS THE THROMBIN-AND PLASMIN-
INDUCED AGGREGATION OF THROMBOCYTES; (4) THE ACTIVE PEPTIDE
RADYKININ THAT IS RELEASED FROM HWW-KININOGEN SHOWS A VARIETY OF
PHYSIOLOGICAL PEPECTS: (4A) INFLUENCE IN SMOOTH MUSCLE
CONTRACTION, (4B) INDUCTION OF HYPOTENSION, (4C) NATRURESIS AND
DIURESIS, (4D) DECREASE IN BLOOD GLUCOSE LEVEL, (4E) IT IS A
MEDIATOR OF INFLAMMATION OF NOCICEPTORS (4B) RELEASE OF
OTHER MEDIATORS OF INFLAMMATION (C. O. PROSTAGLANDINS), (4F) IT HAS
C CARRIOPROTECTIVE EFFECT (DIRECTLY VIA BRADYKININ ACTION,
INDIRECTLY VIA ENDOTHELIUM-DERIVED RELEASING FACTOR ACTION); (5)
LMW-KININOGEN IS IN CONTRAST TO HWM-KININOGEN NOT INVOLVED IN BLOOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Chycoprotein; Plasma; Repeat; Thiol protease inhibitor; Vasodilator; Bradykinin; Blood coagulation; Inflammatory response; Signal; Alternative splicing.

SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                          ALTERNATIVE PRODUCTS: 2 ISOFORMS; HMW (SHOWN HERE) AND LMW; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: PLASMA.
PTM: BRADYKININ IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Secreted.
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ProDom; PD001231; Cystatin_C_M; 1.
SMART; SM00043; CY; 3.
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InterPro; IPR002395; Kininogen.
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InterPro; IPR000010; Cystatin.
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EMBL; M11526, AAB59551.1; JOIN
EMBL; M11528, AAB59551.1; JOIN
PIR; A01279; KGHUH1.
PIR; A01280; KGHUH1.
PIR; A01280; KGHUH1.
PIR; B02576; B25276.
PIR; S02482; S02482.
SWISS-2DPAGE; P01042; HUMAN.
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EMBL; M11437; AAB59550.1; -.
Seikagaku 56:808-808(1984)
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AABS9550 1;
AABS9551 1;
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M11525;
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M11522;
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Nawa H., Kitamura N., Hirose T., Asai M., Inayama S., Nakanishi S.;
"Primary structures of bovine liver low molecular weight kininogen precursors and their two mRNAs.";
Proc. Natl. Acad. Sci. U.S.A. 80:90-94(1983).
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21-JUL-1986 (Rel. 01, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Kininogen, LMW II precursor (Thiol proteinase inhibitor) (Contains: Bradykinin].
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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                                                      KININOGEN LIGHT CHAIN.
CYSTATIN-LIKE 1.
CYSTATIN-LIKE 2.
CYSTATIN-LIKE 3.
CYSTATIN-LIKE 3.
ACTAVITY).
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N-LINKED (GLCNAC. ..) (POTENTIAL)
N-LINKED (GLCNAC. ..) (POTENTIAL)
N-LINKED (GLCNAC. ..) (POTENTIAL)
O-LINKED.

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                                                                                                                                                                                                                                                                                                                                       PYRROLIDONE CARBOXYLIC ACID.
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3132B4CBAF8FBB7E CRC64;
KININOGEN HEAVY CHAIN.
BRADYKININ.
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593
644 AA;
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Best Local Similarity
Matches 32; Conserv
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SEQUENCE FROM N.A.
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P01047;
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Gaps

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Indels

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3; Mismatches

Conservative

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                                                                                                            RESULT 3
KNH2_BOVIN
   Matches
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                                                                                                       J. Biol. Chem. 262:2768-2779(1987).
-!- FUNCTION: (1) KININOGENS ARE INIBITORS OF THIOL PROTEASES; (2)
LAWA-KININOGEN INHIBITS THE AGEREGATION OF THROMBOCYTES; (3) THE
ACTIVE PEPTIDE KALLIDIN THAT IS RELEASED FROM LAWA-KININOGEN SHOWS
A VARLETY OF PHYSIOLOGICAL EFFECTS: (3A) INFLUENCE IN SMOOTH
MUSCLE COMPRACTION, (3B) INDUCTION OF HYPOTENSION, (3C)
NATRIURESIS AND DIURESIS (KIDDRY).
                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Extracellular.

PALERNATIVE PRODUCTS: HWW II AND LAW II KININGEN PRECURSORS ARE PRODUCED FROM THE SAME GENE AS THE RESULT OF ALTERNATE MRNA SPLICING. THE SEQUENCES OF BOTH KININGENS ARE IDENTICAL UP TO RESIDUE 398.
                                                                                                                                                                                                                                                                                            -1- TISSUE SPECIFICITY: PLASMA.
-1- PTM: BRADYKININ IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN.
-1- MISCELLANEOUS: LMW-KININOGEN IS IN CONTRAST TO HMW-KININOGEN NOT
                                           Miyata T., Iwanaga S.;
"Bovine high molecular weight kininogen. The amino acid sequence,
positions of carbohydrate chains and disulfide bridges in the heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00287; CYSTATIN; 2.
Glycoprotein; Plasma; Repeat; Vasodilator; Alternative splicing;
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CYSTATIN-LIKE 2.
CYSTATIN-LIKE 3.
PYRROLIDONE CARBOXYLIC ACID.
N-LINKED (GLCNAC. .).
O-LINKED (GLCNAC. .), OR 169.
N-LINKED (GLCNAC. .), OR 169.
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SEGÜENCE OF 19-376.
MEDILNE-87137530; PubMed-3546295;
SUGYOSAI I., MIYBLA T., HAShimoto N., Kato H., Hayashida H.,
MIYAta T., Iwanaga S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48148 MW; 73A7079DE3E03430 CRC64;
                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
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InterPro; IPR000010; Cystatin.
InterPro; IPR003243; Cystatin_C_M.
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ProDom; PD001231; Cystatin_C_M; 1.
SMART; SM00043; CY; 3.
                                                                                                                                                                                                                                                                                                                                             INVOLVED IN BLOOD CLOTTING
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434 AA;
                                                                                          chain portion."
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Score 116; DB 1; Length 434;

Pred. No. 6e-09;

72.0%; 74.2%;

Best Local Similarity

Query Match

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SEQUENCE OF 492-496.

MEDLINE-75170265; Pubbed=1169237;
Han Y.N., Komiya M., Iwanaga S., Suzuki T.;
Han Y.N., Komiya M., Iwanaga S., Suzuki T.;
Han Y.N., Komiya M., Iwanaga S., Suzuki T.;
Studies on the primary structure of bovine high-molecular-weight
kininogen. Amino acid sequence of a fragment ('histidine-rich
peptide') released by plasma kallikrein.";

U. J. Biochem. 77:55-68[1975].

L. GUNCTION: (1) KININOGENS ARE INHIBITORS OF THIOL PROTEASES; (2)
HAW-KININOGEN PLAYS AN IMPORTANT ROLE IN BLOOD COAGULATION BY
HELPING TO POSITION OPTIMALLY PREKALLIKREIN AND FACTOR XII.

C. PLASMIN-INDUCED AGGREGATION OF THROMBOCYTES; (4) THE ACTIVE
PEPTIDE BRADYKININ THAT IS RELEASED FROM HMW-KININOGEN SHOWS
A VARIETY OF PHYSIOLOGICAL BEFECTS; (4) INFLUENCE IN SMOOTH
MUSCLE CONTRACTION, (4B) INDUCTION OF HYPOTENSION, (4C)
NATRIURESIS AND DIURESIS, (4D) DECREASE IN BLOOD GLUCOSE LEVEL,
(4E) IT IS A MEDIATOR OF INFLAMMATION ND CAUSES (4E1) INCREASE
IN VASCULAR PERMEABILITY, (4E2) STIMULATION OF NOCICEPTORS (4E3)
RELEASE OF OTHER MEDIATORS OF INFLAMMATION (E.G. PROSTAGLANDINS),
(4F) IT HAS A CARDIOPROTECTIVE EFFECT (DIRECTLY VIA BRADYKININ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDILINE-70180420; PubMed-4986212;
MEDILINE-70180420; PubMed-4986212;
Kato H., Nagasawa S., Suzuki T.;
"Studies on the structure of bovine kininogen: cleavages of disulfide bonds and of methionyl bonds in kininogen-II.";
J. Blochem. 67:313-323(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 387-455.

MEDIATE=76260155; PubMed-956151;

MEDIATE=76260155; PubMed-956151;

"Primary structure of bovine plasma high-molecular-weight kininogen."

"Primary structure of bovine plasma high-molecular-weight kininogen. The amino-acid sequence of a glycopeptide portion (fragment 1) (following the C-terminus ot the bradykinin molety.";

J. Biochem. 79:1201-1122(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   positions of carbohydrate chains and disulfide bridges in the heavy
                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
-JUL-1986 (Rel. 01, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Kininogen, HWW II precursor (Thiol proteinase inhibitor) (Contains:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kitamura N., Takagaki Y., Furuto S., Tanaka T., Nawa H., Nakanishi
"A single gene for bovine high molecular weight and low molecular
weight kininogens":
                                                                                                                                                                                                                                                                                                            Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-87137530; PubMed-3546295;
Sueyoshi T., Miyata T., Hashimoto N., Kato H., Hayashida H.,
Miyata T., Iranaga S.;
"Bovine high molecular weight kininogen. The amino acid sequence,
                                                                                                                                                        Æ
                                                                                                                                                        619
                       279 LNHSIAKLNAEHDGTFYFKIDTVKKATVQVV 309
2 LTHTITKLNAENNATFYFKIDNVKKARVQVV 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chain portion.";
J. Biol. Chem. 262:2768-2779(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE-84014106; PubMed-6571699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 305:545-549(1983).
                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          weight kininogens
                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                          Bradykinin].
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P01045;
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P01046;
                         RESULT 4
                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                     SUBCELÍULAR LOCATION: Extracellular.
ALTERNATIVE PRODUCTS: HWM II AND LAW II KININGEN PRECURSORS ARE
PRODUCED FROM THE SAME GENE AS THE RESULT OF ALTERNATE MRNA
SPLICING. THE SEQUENCES OF BOTH KININGENS ARE IDENTICAL UP
                                                                                               -i- PTM: BRADYKININ IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN.
-i- SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                             PROSITE: PROGOS, CYSTATIN; 2.
Glycoprotein; Plasma; Repeat; Vasodilator; Alternative splicing;
Thiol protease inhibitor; Bradykinin; Blood coagulation; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PYRROLIDONE CARBOXYLIC ACID.
N-LINKED (GLCNAC. .).
O-LINKED (PARTIAL).
N-LINKED (GLCNAC. .); OR 169.
N-LINKED (GLCNAC. .); (PARTIAL).
N-LINKED (GLCNAC. .).
ACTION, INDIRECTLY VIA ENDOTHELIUM-DERIVED RELAXING FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72.0%; Score 116; DB 1; Length 619; 74.2%; Pred. No. 8.7e-09; ive 3; Mismatches 5; Indels
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L -> V.
H -> K.
; F04320A8EB0EE0DA CRC64;
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HEAVY CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYSTATIN-LIKE 1.
CYSTATIN-LIKE 2.
CYSTATIN-LIKE 3.
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INTERCHAIN.
                                                                                                                                                                                                                                                        PIR; A01282; KGB0H2.

PIR; B29559; B29559.

INCERP: PO1038; 1A90.

InterPro; IPR00010; Cystatin.

InterPro; IPR003243; Cystatin.

InterPro; IPR003395; Kininogen.
                                                                                                                                                                                                                                                                                                                                Pfam; PF00031; cystatin; 3.
PRINYS; PR00334; KININOGEN.
ProDom; PD001231; Cystatin_C_M; 1.
SMART; SM00043; CY; 3.
                                                                                                                                                                                                                                EMBL; V01492; CAA24736.1; -. EMBL; V01492; CAA24737.1; ALT_SEQ.
                                                                                  TISSUE SPECIFICITY: PLASMA.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a allocanse agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                 AS Suegoshi T., Miyata T., Hashimoto N., Kato H., Hayashida H.,

Miyata T., Iwanaga S.;

Bovine high molecular weight kininogen. The amino acid sequence,

positions of carbohydrate chains and disulfide bridges in the heavy

chain portion.";

J. Biol. Chem. 262:2778(1987).

LAW-KININOGEN INIBITS THE AGREGATION OF THROMBOCYTES; (3) THE

ACTIVE PEPTIDE KALLIDIN THAT IS RELEASED FROM LAW-KININOGEN SHOWS

A VARIETY OF PHYSIOLOGICAL EFFECTS: (3A) INFLUENCE IN SMOOTH

MUSCLE CONTRACTION, (3B) INDCTION OF HYPOTENSION, (3C)

NATRIURESIS AND DIURESIS (KIDNEY).

C. -- SUBCELLUIAR LOCATION: Extracellular.

C. -- ALTERNATIVE PRODUCTS: HWW I AND LAW I KININOGEN PRECURSORS ARE

PRODUCED FROM THE SAME GENER AS THE RESULT OF ALTERNATE MRNA

SPLICIAN...

SPLICIAN...

SPLICIAN...

SELICIAN...

SELICIAN...

AND THE SEQUENCES OF BOTH KININOGEN SAE IDENTICAL UP
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-i- PTM: BRADYKININ IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN.
-i- MISCELLANDEOUS: LAM-KININOGEN IS IN CONTRAST TO HMW-KININOGEN NOT INVOLVED IN BLOOD CLOTTING.
-i- SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-83117859; PubMed-6572010;
Mawa H., Kitamura N., Hirose T., Asai M., Inayama S., Nakanishi S.;
Newa H., Kitamuras of bovine liver low molecular weight kininogen
precursors and their two mRNAs.";
Proc. Natl. Acad. Sci. U.S.A. 80:90-94(1983).
                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 41, Last annotation update)
Kininogen, LMW I precursor (Thiol proteinase inhibitor) [Contains: Bradykinin].
                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00287; CYSTATIN; 2.
Glycoprotein; Plasma; Repeat; Vasodilator; Alternative splicing;
Thiol protease inhibitor; Bradykinin; Signal.
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436 AA.
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BRADYKININ.
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EMBL; J00010; AAA30604.1; -.
PIR; A401283; KGBOL1.
InterPro; IPR00010; Cystatin.
InterPro; IPR003243; Cystatin.C_M.
Pfan; PP00031; cystatin; 3.
ProDom; PD001231; Cystatin, C.M.
SWART; SM00043; CY; 3.
PRT;
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STANDARD;
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NCBI_TaxID=9913;
                                                                                                                                          Bos taurus (Bovine).
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389
KNL1_BOVIN
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Gaps

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279 LNHSIAKLNAEHDGTFYFKIDTVKKATVQVV 309

2 LTHTITKLNAENNATFYFKIDNVKKARVQVV 32

23; Conservative

Matches

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Similarity

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68890 MW;
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MEDLINE-81137530; PubMed-3546295;
Sueyoshi T., Miyata T., Hashimoto N., Kato H., Hayashida H.,
Miyata T., Iwanaga S.;
"Bovine high molecular weight kininogen. The amino acid sequence,
positions of carbohydrate chains and disulfide bridges in the heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
MEDLINE-84014106; PubMed-6571699;
Kitamura N., Takagaki Y., Furuto S., Tanaka T., Nawa H., Nakanishi
"A single gene for bovine high molecular weight and low molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last sequence update)
41-JUAR-2002 (Rel. 41, Last annotation update)
41-JUAR-2002 (Rel. 01, Last annotation update)

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus (Bovine).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthazia; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinee; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 458-498.
MEDLINE=75170265; PubMed=1169237;
Han Y.N., Komlya M., Iwanaga S., Suzuki T.;
"Studies on the primary structure of bovine high-molecular-weight.
   CYSTATIN-LIKE 1.
CYSTATIN-LIKE 2.
CYSTATIN-LIKE 3.
CYSTATIN-LIKE 3.
PYRROLIDONE CARBOXYLIC ACID.
N-LINKED (GLCNAC. . .).
N-LINKED (GLCNAC. . .).
N-LINKED (GLCNAC. . .); OR 169.
N-LINKED (GLCNAC. . .) (PARTIAL).
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Pred. No. 2.2e-08;
4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                      Rato H., Nagasawa S., Suzuki T.;
"Studies on the structure of bovine kininogen: c
bonds and of methionyl bonds in kininogen-II.";
J. Biochem. 67:313-323(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               621 AA
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                                                                                                                                         INTERCHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 378-393.
MEDLINE=70180420; PubMed=4986212;
                                                                                                                                                                                                                                                                                     48427 MW;
                                                                                                                                                                                                                                                                                                                               ch 69.6%;
1 Similarity 71.0%;
22; Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              weight kininogens.";
Nature 305:545-549(1983).
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436 AA;
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CARBOHYD
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PER PRILINGORON. AND CACLE ACCOUNTS. A FRANCES. (1)

REAL STATES - 68 (1972)

REAL STATES - 68 (
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LOCATION: Secreted

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MEDLINE-87137465; PubMed-3818598;

A Rageyama R., Kitamura N., Ohkubo H., Nakanishi S.;

A Rageyama R., Kitamura N., Ohkubo H., Nakanishi S.;

A Rageyama R., Kitamura N., Ohkubo H., Nakanishi S.;

A Biol. Cas. 2346-2331(1987).

A Biol. Chem. 262:2346-2331(1987).

B Biol. Chem. 262:2346-2331(1987).

THORITON: (1) KININOGENS ME INHIBITORS OF THIOL PROTEASES; (2) HWW-KININOGEN PLAYS AN IMPORTANT ROLE IN BLOOD COAGULATION BY HELPIN GT OP DOSTITON OPTIMALLY PREKALLIKREIN AND FACTOR XI IN COSTITON OF THANOMBOLYPES; (4) THE ACTIVE PEPTIDE RACTOR XII; (3) HWW-KININOGEN INHIBITS THE THROMBIN-AND PLASMIN-INDUCED AGGREGATION OF THANOMBOLYPES; (4) THE ACTIVE PEPTIDE PRESIDENCE LEFFECTS: (4A) INFLUENCE IN SMOOTH MOSCLE

CONTRACTION, (4B) INDUCTION OF HYDOTENSION, (4C) NATHURESIS AND DIURESIS, (4D) DECREASE IN BLOOD GLUCOSE LEVEL, (4E) IT IS A MEDIATOR OF INFLAMMATION OF HYDOTENSION, (4C) NATHURESIS AND DIURESIS, (4D) DECREASE IN BLOOD GLUCOSE LEVEL, (4E) IT IS A MEDIATOR OF INFLAMMATION OF NOCICEPTORS (4E3) RELEASE OF OTHER MEDIATORS OF INFLAMMATION OF NOCICEPTORS (4E3) RELEASE OF A CARDIOPROPECTIVE FFEREY (DIRECTLY VIA BRADYKININ ACTION), (5) LAM-KININOGEN IS IN CONTRAST TO HMM-KININOGEN IS IN UNDIRECTLY SOFT INVOLVED IN BLOOD
                                                     ö
                                                     Gaps
                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acute phase alpha 1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-86008264; PubMed-2413018; Pututor-Reto S.; Matsumoto A., Kitamura N., Nakanishi S.; Matsumoto A., Kitamura N., Nakanishi S.; Primary structures of the mRNAs encoding the rat precursors for bradykinin and T-kinin. Structural relationship of kininogens with major acute phase protein and alpha 1-cysteine proteinase inhibitor ".
                                                                                                                                                                                                                                                                                                                                        [1]
SEQUENCE FROM N.A. (ISOFORMS HWW AND LMW).
MEDLINE=87137443; PubMed=3029068;
Kitagawa H., Kitamura N., Hayashida H., Miyata T., Nakanishi S.;
Nitagawa H., Kitamura N., Hayashida H., Miyata T., Nakanishi S.;
"Differing expression patterns and evolution of the rat kininogen
                                                       ö
                       69.6%; Score 112; DB 1; Length 62
71.0%; Pred. No. 3.2e-08;
.ive 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=BUFFALO;
MEDLINE=87250580; PubMed=2439509;
Fung W.-P., Schreiber G.;
"Structure and expression of the genes for major protein (thiostatin) and kininogen in the rat.";
J. Biol. Chem. 262:9298-9308(1987).
                                                                                                                                                                                                          01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
116-OCT-2001 (Rel. 40, Last annotation update)
Kininogen precursor [Contains: Bradykinin].
                                                                                                |:|:| ||||||:
281 LSHSIAKLNAEHDGAFYFKIDTVKKATVQVV 311
                                                                                2 LTHTITKLNAENNATFYFKIDNVKKARVQVV 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biol. Chem. 260:12054-12059(1985).
                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                           Biol. Chem. 262:2190-2198(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (LMW ISOFORM).
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                                                    22; Conservative
                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
                                                                                                                                                                                               P08934; P08933;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inhibitor.
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                                                    Matches
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                                                              -!- TISSUE SPECIFICITY: PLASMA.
-!- PTM: BRADKTKINI IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN.
-!- MISCELLANEOUS: RAT EXPERSS FOUR TYPES OF KININOGENS: THE CLASSICAL.
HMW/LMM KININOGENS AND TWO ADDITIONAL LMM-LIKE KININOGENS: T-I AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VSPSYIARVOEERDPGNEOGPIHGHGWLHAKO -> RLLNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00287; CYSTATIN; 2. Glycoprotein; Plasma; Repeat; Thiol protease inhibitor; Vasodilator; Bradykinin; Blood coagulation; Inflammatory response; Signal; Alternative splicing; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CEYKGRLLKAGAGPAPERQAEASTVTP (IN ISOFORM
                        HMW (SHOWN HERE) AND LMW; ARE
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N-LINKED (GLCNAC. ...) (POTENTIAL).

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Pred. No. 3.3e-08;
2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERCHAIN (BY SIMILARITY).
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D3172DF94FF56AF5 CRC64;
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CYSTATIN-LIKE 1.
CYSTATIN-LIKE 2.
CYSTATIN-LIKE 3.
HIS-RICH.
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                                                                                                                                                                                     SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
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                        ALTERNATIVE PRODUCTS: 2 ISOFORMS; PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; MI1884; AAA41487.1; --
EMBL; M14369; AAA41484.1; --
EMBL; M14369; AAA41485.1; ALT_SEQ.
EMBL; M16455; AAA41482.1; --
PIR; A25486; A25486
PIR; A26485; A26955.
HSSP; P01040; IDVD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00031; cystatin; 3.
PRINTS; PR00334; KININOGEN.
ProDom; PD001231; Cystatin_C_M; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000010; Cystatin.
InterPro; IPR003243; Cystatin_C_M.
InterPro; IPR002395; Kininogen.
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61
639 AA;
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ALTERNATIVE
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Best Local Simi
Matches 23;
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DOMAIN
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HISCELLANDOUS: RAT EXPRESS FOUR TYPES OF KININOGENS: THE CLASSICAL HWW AND LWW KININOGENS PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE, AND TWO ADDITIONAL LWW-LIKE KININOGENS: T-I AND T-II.

CAUTION: IN ADDITION TO THE CONFLICTS DESCRIBED IN THE FEATURE TABLE, REF. 2. SEQUENCE DIFFERS FROM THAT SHOWN IN POSITIONS: 257, 262, 268, 269, 299, 314, 315, 331, 332, AND 389. IN ALL THOSE POSITIONS THE ALTERNATE AMINO-ACID IS THE ONE PRESENT IN T-II KININOGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cole T., Inglis A.S., Roxburgh C.M., Howlett G.J., Schreiber G.; "Major acute phase alpha 1-protein of the rat is homologous to bovine kininogen and contains the sequence for bradykinin: its synthesis is regulated at the mRNA level."; FEBS Lett. 182:57-61(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T-KININGEN I IS RAISED.

PTM: AS T-KININ IS PRECEDED BY A MET INSTEAD OF AN ARG OR LYS, IT IS NOT RELEASED FROM ITS PRECURSOR BY EITHER TISSUE OR PLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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-!- TISSUE SPECIFICITY: PLASMA.
-!- INDUCTION: IN RESPONSE TO AN INFLAMMATORY STIMULANT. T-KININGEN
II SYNTHESIS IS INDUCED AND THE PLASMA CONCENTRATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Furuto-Kato S., Matsumoto A., Kitamura N., Nakanishi S.;
"Primary structures of the mRNAs encoding the rat precursora for
bradykinin and T-kinin. Structural relationship of kininogens with
major acute phase protein and alpha 1-cysteine proteinase
                                                                                                                                                                                                                                                                         01-NOV-1986 (Rel. 03, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
T-kininogen I precursor (Major acute phase protein) (Alpha-1-MAP)
(Thiostatin) [Contains: T-kinin].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anderson K.P., Heath B.C.; The relationship between rat major acute phase protein and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 5-430 FROM N.A., AND PARTIAL SEQUENCE. MEDLINE-86008266; Pubmed-2413019;
                                                                                                                                                                                                                    430 AA.
                                  LTHTITKLNAENNATFYFKIDNVKKARVQVV 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Blol. Chem. 260:12065-12071(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biol. Chem. 260:12054-12059(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-86008264; Pubmed-2413018;
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                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
                                                                                                                                                                                                             KNT1_RAT
PO1048; PO4081;
01-NOV-1986 (Rel
01-NOV-1988 (Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KALLIKREIN
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2
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                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00287; CYSTATIN; 2.
Glycoprotein; Plasma; Repeat; Vasodilator; Multigene family;
Thiol protease inhibitor; Bradykinin; Acute phase; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KED (GLCNAC. . . ) (PO' > MDR (IN REF. 2). (IN REF. 2). (IN REF. 1). (IN REF. 3). (IN REF. 2 AND 3). (IN REF. 2).
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P -> S (IN REF. 1).
FAEBB78FAF4723C3 CRC64;
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SK -> TN (IN REF. 2).

R -> Q (IN REF. 2).

R -> G (IN REF. 2).

A -> L (IN REF. 2).
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N-LINKED (GLCNAC. . .)
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S -> F (IN REF. 2).

R -> H (IN REF. 2).

H -> Y (IN REF. 2).

E -> S (IN REF. 2).

N -> K (IN REF. 2).

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R -> F (IN REF. 2).

I -> L (IN REF. 2).
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CYSTATIN-LIKE 1.
CYSTATIN-LIKE 2.
CYSTATIN-LIKE 3.
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HEAVY CHAIN.
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DH -> ER (
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C - > Y
S - > F
REV - >
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                                                                                                                                                 M16454; MA441570.1; - X02299; CAA7616.1; A01176.1; A01176.1; A01176.1;
                                                                                                                                                                                                                                                                                                                           Pfam; PF00031; cystatin; 3
ProDom; PD001231; Cystatin
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CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MISCELLANEOUS: RAT EXPRESS FOUR TYPES OF KININGGENS: THE CLASSICAL HAW AND LAW KININGGENS PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE, AND TWO ADDITIONAL LAW-LIKE KININGGENS: T-I AND T-II. SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- FUNCTION: KININGGENS ARE PLASMA GLYCOPROTEINS WITH A NUMBER OF FUNCTIONS: (1) AS PRECURSOR OF THE ACTIVE PEPTIDE BRADYKININ THEY EFFECT SMOOTH MUSCLE CONTRACTION, INDUCTION OF HYPOTENSION AND INCREASE OF VASCULAR PERMEABILITY. (2) THEY PLAY A ROLE IN BLOOD COAGGILATION BY HELPING TO POSTITION OPTIMALLY PREKALLIKREIN AND FACTOR XI NEXT TO FACTOR XII. (3) THEY ARE INHIBITOR OF THIOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE SPECIFICITY: PLASMA.

INDUCTION: IN RESPONSE TO AN INFLAMMATORY STIMULANT. T-KININOGEN
IN SYMPHESIS IS INDUCED AND THE PLASMA CONCENTRATION OF
T-KININOGEN I IS RAISED.
PTM: AS T-KININ IS PRECEDED BY A MET INSTEAD OF AN ARG OR LYS, IT
IS NOT RELEASED FROM ITS PRECURSOR BY EITHER TISSUE OR PLASMA
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Furuto-Kato S., Matsumoto A., Kitamura N., Nakanishi S.; "Primary structures of the mRNAs encoding the rat precursors for bradykinin and T-kinin. Structural relationship of kininogens with
                                                                                                                                                                                                                                                                                                                                 01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
T-kininogen II precursor (Major acute phase protein) (Alpha-1-MAP)
(Thiostatin) [Contains: T-kinin].
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Thiol protease inhibitor; Bradykinin; Acute phase; Signal.
SIGNAL
               Score 98; DB 1; Length 430;
Pred. No. 2e-06;
4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               major acute phase protein and alpha 1-cysteine proteinase
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                                                                                                                                                                                                                                                                                            430 AA.
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                                                                                                                                                 281 LGHSIAQLNAQHNHIFYFKIDTVKKATSQVV 311
                                                                                                                   2 LTHTITKLNAENNATFYFKIDNVKKARVQVV 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Biol. Chem. 260:12054-12059(1985).
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PIR; B28055; B28055
G1ycoSuiteDB; P08932; -.
InterPro; IPR000010; Cystatin.
InterPro; IPR003243; Cystatin.
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                    60.9%;
64.5%;
                                             Local Similarity 64.5
les 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                         STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
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                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 kininogen.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: (1) KININOGENS ARE INHIBITORS OF THIOL PROTEASES; (2)
--HWW-KININOGEN PLAYS AN IMPORTANT ROLE IN BLOOD COAGULATION BY
HELPING TO POSITION OPTIMALLY PREKALLIKREIN AND FACTOR XI NEXT TO
FACTOR XII; (3) HWW-KININOGEN INHIBITS THE THROMBIN-AND PLASMIN-
INDUCED AGGREGATION OF THROMBOCYTES; (4) THE ACTIVE PEPTIDE
BRADYKININ THAT IS RELEASED FROM HWW-KININOGEN SHOWS A VARIETY OF
PHYSIOLOGICAL EFFECTS: (4A) INFLUENCE IN SMOOTH MUSCLE
CONTRACTION, (4B) INDUCTION OF HYPOTENSION, (4C) NATRIURESIS AND
DIURESIS, (4D) DECREASE IN BLOOD GLUCOSE LEVEL, (4E) IT IS A
MEDIATOR OF INFLAMMATION AND CAUSES (4E1) INCREASE IN VASCULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; HWW (SHOWN HERE) AND LMM; ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: PLASMA.
                                                                                                                                                    INTERCHAIN (BY SIMILARITY).

BY SIMILARITY.

N-LINKED (GLCNAC. ...) (POTENTIAL).

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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STRAIN-CS/BL/C & CBA; TISSUE-LIVEY;
TAKANO M., KONGON J., Yayama K., Okamoto H.;
"Molecular cloning of cDNAs for mouse low- and high- molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60.9%; Score 98; DB 1; Length 430;
llarity 64.5%; Pred. No. 2e-06;
Conservative 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43EDF02D1BF55076 CRC64;
                                               LIGHT CHAIN.
CYSTATIN-LIKE 1.
CYSTATIN-LIKE 2.
CYSTATIN-LIKE 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KNG_MOUSE STANDARD; PRT; 661 AA. 008677; 008676; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Kininogen precursor [Contains: Bradykinin].
HEAVY CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               281 LGHSIAQLNAQHNHLFYFKIDTVKKATSQVV 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 LTHTITKLNAENNATFYFKIDNVKKARVQVV 32
                            T-KININ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MW;
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Best Local Similarity
Matches 14; Conserv
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                                                                             SEQUENCE FROM N.A.
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                                               NCBI_TaxID=10090;
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Q9VTF9;
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CEYKGRLSKAGAEPAPERQAESSQVKQ (IN ISOFORM
                                                                                                                                                                                                                                                                                  PROSITE; PS00287; CYSTATIN; 1.
Glycoprotein; Plasma; Repeat; Thiol protease inhibitor; Vasodilator; Alternative splicing.
Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
- 14 PTM: BRADYKININ IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN.
-1- SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                               KININGGEN LIGHT CHAIN.
CYSTATIN-LIKE 1.
CYSTATIN-LIKE 2.
CYSTATIN-LIKE 3.
HIS-RICH.
INTERLARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTE_MOUSE STANDARD; PRT; 144 AA.
089036;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Cystatin F precursor (Leukocystatin) (Cystatin 7) (Cystatin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 98; DB 1; Lengtn vo., Pred. No. 3.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MISSING (IN ISOFORM LMW). 774460258D58796E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        KININOGEN.
KININOGEN HEAVY CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       BRADYKININ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  metastasis-associated protein) (CMAP)
                                                                                                                                                               EMBL; D84435; BAA19743.1; -.
EMBL; D84415; BAA19742.1; -.
MGD; MGI:1097705; Rng.
InterPro; IPR000010; Cystatin.
InterPro; IPR003243; Cystatin_C_M.
InterPro; IPR003243; Kininogen.
Pfam; PF00031; cystatin; 3.
PRINTS; PR00334; KINTNOGEN.
ProDom; PD001231; Cystatin_C_M; 1.
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73102 MW;
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64.5%;
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379
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661 AA;
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Best Local Similarity
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                           MEDLINE-98298157; PubMed-9632704;
Halfon S., Ford J., Foster J., Dowling L., Lucian L., Sterling M.,
Xu Y., Welss M., Ikeda M., Liggett D., Helms A., Caux C., Lebecque S.,
Hannum C., Wenson S., McClanahan T., Gorman D., Zurawski G.;
Leukocystatin, a new class II cystatin expressed selectively by
hematopoietic cells.";
J. Biol. Chem. 273:16400-16408(1998).
I- FUNCTION: INILIBITS PAPAIN AND CATHEPSIN L BUT WITH AFFINITIES
LOWER THAN OTHER CYSTATINS. MAY PLAY A ROLE IN IMMUNE REGULATION
THROUGH INHIBITION OF A UNIQUE TARGET IN THE HEMATOPOIETIC SYSTEM.
-! SUBCELLULAR LOCATION: Secreted (Probable).
-! SIBLIARITY: BELONGS TO THE CYSTATIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Ubiquitin fusion degradation protein 1 homolog (UB fusion protein CG6233.
Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REACTIVE SITE.
SECONDARY AREA OF CONTACT.
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Thiol protease inhibitor; Glycoprotein; Signal.
SIGNAL 1 18 CYSTATIN F.
CYSTATIN 19 144 CYSTATIN F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       316 AA.
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BY SIMILARITY.
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InterPro; IRRO00010; Cystatin.
InterPro; IRRO03143; Cystatin_C_M.
Pfam; PF00031; cystatin; I.
ProDom; PD001231; Cystatin_C_M: SWART; SMO043; Cystatin_C_M; Cysta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 HTITKLNAENNATFYFKIDNVKKARVQVV 32
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Heat shock protein 83 (HSP 83).
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R.A. Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
R.A. Amanatides D.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
R.A. George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X.,
R.A. Bardon R.C., Baxter E.G., Helt G., Noblson C.R., Miklos G.L.G.,
R.A. Ballew R.M., Basu A. B. Barenson E.S., Helt G., Noblson C.R., Miklos G.L.G.,
R.A. Beson K.Y., Bencs P.V., Berman B.P., Bhandari D., Bolshakov S.,
R.A. Berson K.Y., Bencs P.V., Berman B.P., Bhandari D., Bolshakov S.,
R.A. Burtis K.C., Busam D.A., Bulke C., Davenport L.B., Davies P.,
R. Burtis R.C., Busam D.A., Bulke C., Davenport L.B., Davies P.,
R. Burtis R.C., Eusam D.A., Bulke C., Davenport L.B., Davies P.,
R. Burtis R.C., Edbriellan A.E., Garty N.S., Galbart W.M., Glasser K.,
R. Ballon K.J. Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
R.A. Bartis N.L., Evangelista C.C., Ferraz C., Ferriera S., Pleischman W.,
R.A. Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeqwam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kalub D., Lai Z.,
R. Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeqwam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Gelbert W. Pouck J.,
R. Mimel B.E., Kodirac C.D., Kraft C., Kraft 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ubiquitin conjugation.
SEQUENCE 316 Aa; 34791 MW; B7C1EA88CCA5CDA3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 52; DB 1;
Pred. No. 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 23, Created)
(Rel. 23, Last sequence update)
(Rel. 27, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
 MEDLINE=20196006; PubMed=10731132;
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50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 287:2185-2195(2000).
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Best Local Similarity
Matches 12; Conserva
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01-AUG-1992 (
01-OCT-1993 (
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F27741;
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                             Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gentles S., Churcher C.M., Barrell B.G., Rajandream M.A., Wood V.; Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                       Shapria M., Pedraza G.;
"Sequence analysis and transcriptional activation of heat shock protein 83 of Leishmania mexicana amazonensis.";
Mol. Blochem. Parasitol. 42:247-256(1990).
-:- FUNCTION: MOLECULAR CHAPERONE. HAS ATPASE ACTIVITY
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 52; DB 1; Length 701; Pred. No. 9.4; 6; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00298; HSP90; 1.
Chaperone; ATP-binding; Heat shock.
SEQUENCE 701 AA; 80584 MW; 05100A1324A80812 CRC64;
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Hypothetical 35.8 kDa protein C4F8.04 in chromosome I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schlzosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       306 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TLTHTITKLNAENNATFYFKIDNVKK 26
                                                                                                                       SEQUENCE FROM N.A.
STRAIN-ISOLATE MHOM/BR/77/LTB0016;
                                                                                                                                                                                    MEDLINE=91101661; PubMed-2270107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P07900; IYER.
InterPro; IPR003594; HATPase_c.
InterPro; IPR001404; HSP90.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PR00775; HEATSHOCK90.
SM00387; HATPase_c; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF02518; HATPase_c; 1.
Pfam; PF00183; HSP90; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
Leishmania amazonensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : A44943; A44943.
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                          NCBI_TaxID=5659;
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DISULFID
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Best Local $
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Falquerho L., Patey G., Paqureau L., Rossi V., Lahuna O., Szpirer J., Szpirer C., Levan G., Le Cam A.;
"Primary structure of the rat gene encoding an inhibitor of the Insulin receptor tyrosine kinase.";
Gene 98:209-216(1991).
                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-92174906; PubMed=1371750;
MEDLINE-92174906; PubMed=1371750;
MEDLINE-92174906; PubMed=1371750;
Hacring H., Nawratil P., Haasemann M., Jahnen-Dechent W.,
Mueller-Esterl W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Molecular cloning and sequence analysis of cDNA for a 59 kD bone sialoprotein of the rat: demonstration that it is a counterpart of human alpha 2-HS glycoprotein and bovine fetuin.";
J. Bone Miner. Res. 8:367-377(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ul-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Alpha-2-HS-glycoprotein precursor (Fetuin-A) (Glycoprotein PP63)
(59 kDa bone sialic acid-containing protein) (BSP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Auberger P., Falquerho L., Contreres J.O., Pages G., le Cam G., Rosal B., le Cam A.; "Characterization of a natural inhibitor of the insulin receptor tyrosine kinase: cDNA cloning, purification, and anti-mitogenic
                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The nucleotide and partial amino acid sequences of rat fetuin Identity with the natural tyrosine kinase inhibitor of the rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ohnishi T., Nakamura O., Ozawa M., Arakaki N., Muramatsu T., Dalkuhara Y.;
                                                                                                                                                                                                                                Score 50; DB 1; Length 306;
Pred. No. 7.4;
                                                                                                                                                     al protein.
306 AA; 35835 MW; 2029FBB2358EC01E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             352 AA
                                                                                                                                                                                                                                                                    9; Mismatches
                                                                                                                                                                                                                                                                                                                              insulin_receptor.";
Eur. J. Biochem. 204:523-529(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                        3 THTITKLNAENNATFYFKIDNVKKAR 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE-93206661; Pubmed-7681247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REVISIONS, SEQUENCE FROM N.A. MEDLINE-91200667; PubMed=1849862;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-89354538; PubMed-2766355;
                                                                                         EMBL; 298530; CAB11051.1; -. InterPro; IPR002799; IMP4. Pfam; PF01945; IMP4; 1. Hypothetical protein.
                                                                                                                                                                                                                                31.1%;
30.8%;
                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cell 58:631-640(1989)
                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                              Query Match
Best Local Si
Matches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                           A2HS_RAT
P24090;
                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
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CELL 68:7-8(1992).

CELL 68:7-8(1992).

CONCOMITANTLY, ANTAGONIZE THE MITOGENIC EFFECT OF THE HORMONE IN COULUNED RAT HEPATOMA CELLS.

CONCOMITANTLY, ANTAGONIZE THE MITOGENIC EFFECT OF THE HORMONE IN COLLURED RAT HEPATOMA CELLS.

CILTURED RAT HEPATOMI SECRETED BY THE HEPATOCYTES IN THE BLOOD.

CILTURED SPECIFICITY: SYNTHESIZED IN LIVER AND SECRETED BY THE HEPATOCYTES IN THE BLOOD.

CILTURED RATION, AND ADDITION OF FUCOSE AND SIALIC ACID RESIDUES.

PHOSPHORYLATION, AND ADDITION OF FUCOSE AND SIALIC ACID RESIDUES.

CHOSPHORYLATION, AND ADDITION FAMILY.

CHOSPHORYLATION COCURS AT A SERINE RESIDUE.

CHOSPHORYLATION COCURS AT A SERINE RESIDUE.

CHOSPHORYLATION OCCURS AT A SERINE RESIDUE.
                                                                                                                                                                                                            MEDLINE-92119718; PubMed-1370655; Brown W.M., Christie D.L., Dziegielewska K.M., Saunders N.R., Yang F.; Brown W.M., Christie D.L., Dziegielewska K.M., Saunders N.R., Yang F.; "The rat protein encoded by clone pp63 is a fetuin/alpha 2-HS glycoprotein-like molecule, but is it the tyrosine kinase inhibitor pp63?";
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IDENTITY OF PP63 WITH FETUIN.
MEDLINE=91190111; PubMed=1707273;
Haasemann M., Nawratil P., Mueller-Esterl W.;
"Rat tyrosine kinase inhibitor shows sequence similarity to human alpha 2-HS glycoprotein and bovine fetuin.";
Biochem. J. 274:899-902(1991).
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N-LINKED (GLCNAC. . . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
CLEAVAGE (BY TRYPEIN) (POTENTIAL).
CLEAVAGE (BY TRYPEIN) (POTENTIAL).
D -> H (IN REF. 2 AND 3).
E -> Q (IN REF. 2 AND 3).
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-> Q (IN REF. 2 AND 3).
43564F60F3C7C90A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYSTATIN-LIKE 1. CYSTATIN-LIKE 2.
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InterPro; IPR001363; Fetuin.
Pfam; PF00031; cystatin; 2.
SMART; SM00043; CY; 2.
PROSITE; PS01254; FETUIN_1; 1.
PROSITE; PS01255; FETUIN_2; 1.
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EMBL; X63446; CAA45042.1; -..
EMBL; D10261; BAA01101.1; -..
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35.7%;
                                                                                                                                                                                        IDENTITY OF PP63 WITH FETUIN.
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PIR; S22382; S22382
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76
352 AA;
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1457
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                                                                                                                                                                                                                                                                                                                         Kulakauskas S., Barsonian J.M., Lubys A., Roberts R.J., Wilson G.G.; "Organization and sequence of the Hpall restriction-modification system and adjacent genes."; Gene 142:9-15(1994).

-I- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE CGG AND CLEAVES AFTER C-1.

-I- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give specific double-stranded fragments with terminal 5' phosphates.
                                                    01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
17ype II restriction enzyme HpaII (EC 3.1.21.4) (Endonuclease HpaII)
(R.HpaII).
                                                                                                                                                                    Haemophilus parainfluenzae.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30.4%; Score 49; DB 1; Length 358; 38.5%; Pred. No. 12; tive 5; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase; Endonuclease; Nuclease; Restriction system.
SEQUENCE 358 AA; 40925 MW; ECB312180C80303E CRC64;
                  358 AA.
                  PRT;
                                                                                                                                                                                                                                                                                       STRAIN-ATCC 4969;
MEDLINE-94237495; PubMed-7514149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L17342; AAA20482.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 30.4
Best Local Similarity 38.5
Matches 10; Conservative
                  STANDARD;
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                NCBI_TaxID=729;
                T2H2_HAEPA
P36433;
T2H2_HAEPA
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Search completed: July 1, 2002, 16:30:13 Job time: 622 sec

7 TKLNAENNATFYFKIDNVKKARVQVV 32

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Gaps

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P.

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

July 1, 2002, 16:20:36; Search time 46.58 Seconds (without alignments) 24.755 Million cell updates/sec Run on:

US-09-461-061A-2 60 Perfect score: Title:

1 TLTHTITKLNAE 12 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283138 seqs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pir1:\* pir2:\* pir3:\* PIR\_71:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	kininogen, LMW prekininogen, LMW prekininogen, LMW I pkininogen, LMW I pkininogen, LMW I pkininogen, LMW II gene VGF protein ethinogen, HMM II VGFB protein precomplement C3 - ax hypothetical proteconserved hypothetical proteconserved hypothetical protempts on the probable competence methionyl-tRNA for a probable competence probable competence hypothetical protempts a probable competence hypothetical protempts a probable competence hypothetical protempts a probable antioxida heat shock protein genome polyprotein nonstructural protempts of the probable two-compoprobable transcrip K-kininogen, LMW I K-kininogen LMW I K-K-M-MA I LMW I K-K-M-MA I LMW I LM LM I LM	
SUMMARIES	11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	,
	KGHULI KGHULI KGBOLZ 156530 KGBOLZ 156530 KGBOLZ S05381 S05381 S05381 S05381 A10618 A10618 A11718 A24803 S05067 A6515 A6515 A6515	
DB		ı
Length	644 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	
s Query Match	00000000000000000000000000000000000000	
Score		
Result No.	11111111111111111111111111111111111111	

DNA repair protein	hypothetical prote	hypothetical prote	kininogen, HMW I p	polyprotein - hepa	unknown protein, 3	polypeptide - hepa	DNA mismatch repai	alpha,alpha-trehal	hypothetical prote	genome polyprotein					
D86732	C82279	T27077	A25486	JQ1366	F86457	PC2219	A97750	S54500	B98047	GNWVIC	GNWVCJ	A45573	S18030	GNWVTW	GNWVCH
7	7	7	~	~	7	7	7	7	7	Н	Н	Н	Н	<del>1</del>	7
555	589	613	639	716	781	876	890	1211	2551	3010	3010	3010	3010	3010	3011
58.3	58.3	58.3	58.3	58.3	58.3	58.3	58.3	58.3	58.3	58.3	58.3	58.3	58.3	58.3	58.3
35	32	35	32	35	35	35	35	35	35	32	35	35	35	35	35
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

KGHULL  Kininogen, LMW precursor [validated] - human N;Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen N;Contains: bradykinin (kallidin); kininogen I; kininogen II; prokininogen C;Species: Homo sapiens (man) C;Date: 06-Jul-1982 #sequence_revision 27-Nov-1985 #text_change 08-Dec-2000 C;Accession: A01280; B25276; A27900; A27699; A31905; A34030 R;Ohkubo, II; Kurchil, K; Takasawa, T.; Shiokawa, H.; Sasaki, M.	A; Title: Isolation of a human cDNA for alpha-2-thiol proteinase inhibitor and its ide A; Reference number: A90490; MUID:85122621 A; Accession: A01280 A; Molecule type: mRNA A; Residues: 1.427 < COHK>	A;Cross-references: GB:KO2566; NID:g177889; PIDN:AAA35497.1; PID:g177890 R;Takagaki, Y.; Kitamura, N.; Nakanishi, S. J. Biol. Chem. 260, 8601-8609, 1988 A. Biol. Chem. 260, 8601-8609, 1988 A. Biol. Chem.	A;ille: Clouding and Sequence analysts of Comes for maken ingli molecular weight and A;Reference number: A92544; MUID:85234582 A;Accession: B25276
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A Accession: B25276
A Accession: B25276
A Accession: B25276
A Accession: B25276
A Molecule type: mRNA
A; Residues: 1-427 < CTAKA
A; Residues: 1-427 < CTAKA
A; Coss-references: GB:M11437; NID:g186751; PIDN:AAB59551.1; PID:g386853
R; Cottspelich, F: Kellermann, J: Henschen, A:; Rauth, G:; Muculer-Esterl, W.
In Kinins IV, part A, Greenbaum, L.M., and Margollus, H.S., eds., pp.91-95, plenum, N.
A; Title: Amino acid sequence of the light chain of human low molecular mass kininogen
A; Reference number: A27900
A; Molecule type: protein
A; Residues: 390-427 < CLOTO
A; Residues: 300-427 < CLOTO
A; Residues: 300-427 < CLOTO
Biochem. Biophys. Res. Commun. 152, 519-526, 1988
A; Title: A new Kinin molety in human plasma kininogens.
A; Reference number: A27699; MUID:88209021
A; Accession: A27699
A; Molecule type: protein
A; Residues: 380-389 < MIN>
B; Macda, H; Matsumura, Y; Kato, H.
J. Biol. Chem. 263, 16051-16054, 1988
A; Title: Purification and identification of [hydroxyprolyl(3)]bradykinin in ascitic f
A; Reference number: A31905; MUID:89034061
A; Accession: A31905

A;Residues: 381-389 < MAE.
R;Sasaguri, M.; Ikeda, M.; Ideishi, M.; Arakawa, K.
Biochem. Biophys. Res. Commun. 150, 511-516, 1988
A;Title: Identification of [hydroxyproline(3)]-lysyl-bradykinin released from human p A;Reference number: A34030; MUID:88106632 A; Molecule type: protein

A; Molecule type: protein A; Residues: 380-389 <SAS>

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A; Molecule type: protein
A; Residues: 'Z', 20-380 <KEL1>
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A; Residues: 380-389 <KAT1>
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A; Residues: 381-389 <KAT2>
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                                                                                                                                                                                               A; Accession: S32422
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R;Kitamura, N.; Kitagawa, H.; Fukushima, D.; Takagaki, Y.; Miyata, T.; Nakanishi, S. J., Błol. Chem. 250, 8610-96617, 1985
A;Title: Structural organization of the human kininogen gene and a model for its evoluti A;Reference number: A92545; MUID:85234583
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NiAlternate names: alpha-2-thiol proteinase inhibitor; preprokininogen; prokininogen
NiAlternate names: alpha-2-thiol proteinase inhibitor; preprokininogen; prokininogen
NiContains: bradykinin (kallidin I); HWW kininogen I; HWW kininogen II; low molecular we
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens
C; Species: A9115; A9115; A2689; A27699; A31905; A34030; SOZ
R; Ohkubo, I; Kurachi, K; Takasawa, T; Shiokawa, H; Sasaki, M.
A; Ohkubo, I; Kurachi, K; Takasawa, T; Shiokawa, H; Sasaki, M.
A; Jille: Isolation of a human cDNA for alpha-2-thiol proteinase inhibitor and its identi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNAs for human high molecular weight and low
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A;Residues: 1-592,'I',594-644 <TAK>
A;Cross-references: GB:M11437; NID:9186751; PIDN:AAB59550.1; PID:9386852
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                                                                                                                                                                            A)Contents: annotation; gene organization
R;Pierce, J.V.
Fed. Proc. 27, 52-57, 1968
A;Title: Structural features of plasma kinins and kininogens.
A;Reference number: A91455; MUID:90255622
A;Contents: annotation; bradykinin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-389 < COHK>
A; Cross-references: GB: K02566; NID: g177889
F; Takagaki, Y:; Kitamura, N.; Nakanishi, S.
J. Biol. Chem. 260, 8601-8609, 1985
A; Title: Cloning and sequence analysis of c.
A; Reference number: A92544; MUID: 85234582
A; Accession: A25276
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281 TLTHTITKLNAE 292
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A;Molecule type: protein
A;Residues: 380-389 <MIN>
K;Meded, H.; Matsumura, Y.; Kato, H.
J. Biol. Chem. 263, 16051-16054, 1988
A;Title: Purification and identification of [hydroxyprolyl(3)]bradykinin in ascitic f
A;Reference number: A31905; MUID:89034061
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A;Residues: 381-389 <MAE>
R;Sasaguri, M.: Ikeda, M.: Ideishi, M.; Arakawa, K.
Biochem. Biophys. Res. Commun. 150, 511-516, 1988
A;Title: Identification of [hydroxyproline(3)]-lysyl-bradykinin released from human p
A;Reference number: A34030; MUID:88106632
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A; Residues: 1-19;189-192;310-314;381-389 <LEN1>
K; Katco, H.; Matsumura, Y.; Maeda, H.
FEBS Lett. 232, 252-254, 1988
A; Title: Isolation and identification of hydroxyproline analogues of bradykinin in hu
A; Reference number: A61495; MUID:88211869
                                                                                                                                                                                                                                                                                                                                                                            Ricottspeich, F.; Kellermann, J.; Henschen, A.; Foertsch, B.; Muller-Esterl, W. Bur. J. Biochem. 152, 307-314, 11985
A;Title: The amino acid sequence of the light chain of human high-molecular-mass kini A; Reference number: A91153; MUID:86030270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein
A; Residues: 379-644 (LOT>
A; Note: the bradykinin sequence preceding the light chain sequence was not determined
R; Kellermann, J.; Lottspeich, F.; Henschen, A.; Mueller-Esterl, W.
Eur. J. Blochem. 154, 471-478, 1986
A; Title: Completion of the primary structure of human high-molecular-mass kininogen.
A; Reference number: A24871; MUID:86108361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Kellermann, J.; Lottspeich, F.; Henschen, A.; Mueller-Esterl, W. in Kinins IV, Greenbaum, L.M., and Margolius, H.S., ed., pp.85-89, Plenum Press, New A;Title: Amino acid sequence of the light chain of human high molecular mass kininoge
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A; Residues: 380-389 (-385)
R; Lenarcic, B.; Gabrijelcic, D.; Rozman, B.; Drobnic-Kosorok, M.; Turk, V.
Biol. Chem. Hoppe-Seyler 369, 257-261, 1988
A; Title: Human cathepsin B and cysteine proteinase inhibitors (CPIs) in inflammatory
A; Reference number: $02482; MUID: 89076517
                                                                                                 ۳.
R; Auerswald, E.A.; Roessler, D.; Mentele, R.; Assfalg-Machleidt, I.
FEBS Lett. 311, 93-97, 1993
A;Title: Cloning, expression and characterization of human kininogen domain
A;Reference number: $32422; MUID:93223854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein A; Molecule type: protein A; Molecule type: protein A; Residues: 379-389, K', 390-407, Q', 409-644 (KEL2> R; Mindroiu, T.; Carretero, O.A.; Proud, D.; Walz, D.; Scicli, A.G. Biochem. Biophys. Res. Commun. 152, 519-526, 1988 A; Title: A new Kinin molety in human plasma kininogens. A; Reference number: A27699; MUID:88209021 A; Accession: A27699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             this peptide had Pro-383 modified to 4-hydroxyproline ion: C61495
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                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 'ANSM',253-377 <AUE>
A;Note: differences are due to known cloning artifacts
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kininogen, HMW I precursor - bovine
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Matches 8; Conservative
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281 LSHSIAKLNAE 291
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A.Title: Structural features of plasma kinins and kininogens.
A.Fitle: Structural features of plasma kinins and kininogens.
A.Feference number: A01455; MUID:90255622
A.Contents: annotation; bradykinin
C;Comment: The HMW kininogen precursor and the LMW form are produced from the same gene
C;Comment: Kininogen is a cystelahe protechanse inhibitor, takes part in initiation of the
C;Comment: The glycine/histidine/lysine-rich region of HWW kininogen light chain is impo
C;Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator, i
C;Genetics:
A;Gene: GDB:KNG
A;Cross-references: GDB:125256; OMIM:228960
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F.264-375/Domain: cystatin homology <CY2>
F.264-375/Domain: cystatin homology <CY2>
F.264-375/Domain: cystatin homology <CY3>
F.264-375/Domain: cystatin homology <CY3>
F.264-375/Domain: cystatin homology <CY3>
F.380-644/Domain: bradykinin (kallidin I) #status experimental <BDY>
F.380-644/Domain: HWW kininogen light chain #status experimental <br/>F.41-510/Region: glycine/histidine/lysine-rich 30-residue repeats
F.41-434/Product: low molecular weight growth promoting factor #status experimental <GF F.19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experiment F.18/F4/Binding site: carbohydrate (Asn) (covalent) #status experimental F.379-380/Cleavage site: Att. (kallikrein) #status experimental F.379-380/Cleavage site: Att. (kallikrein) #status experimental F.389-390/Cleavage site: Arg-Ser (kallikrein) #status experimental F.389-390/Cleavage site: Arg-Ser (kallikrein) #status experimental F.401,533,542,546,557,571,593,628/Binding site: carbohydrate (Thr) (covalent) #status experimental F.577/Binding site: carbohydrate (Ser) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                         A; Molecule type: protein

A; Mesiduces: 264-359, N°, 361-375 <LEN2>

R; Little, S.S.; Johnson, D.A.

Biochem. J. 307, 341-346, 1995

A; Title: Human mast cell tryptase isoforms: separation and examination of substrate-spectal; R; Reference number: S55239; MUID:95251593

A; Accession: S55239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 431-434 <STR>
N; Kitemura, N; Kitagawa, H; Fukushima, D.; Takagaki, Y.; Miyata, T.; Nakanishi, S.
J; Biol. Chem. 260, 8610-8617, 1985.
A; Title: Structural organization of the human kininogen gene and a model for its evolutines have number: A92545; MUID:85234583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A Map position: 3427-3427
A introns: 65/3: 102/3: 131/1: 188/3: 224/3: 253/1; 310/3; 346/3: 375/3
C: Superfamily: kininogen: cystatin homology
C: Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; dupl
F: 1-18/Domain: signal sequence #status experimental <SIG>
F: 19-64/Product: HWW kininogen I (prokininogen) #status experimental <MATI>
F: 19-379,300-644/Product: HWW kininogen heavy chain #status experimental <MATI>
F: 19-379/Domain: cystatin homology <CYI>
F: 19-11/Domain: cystatin homology <CYI>
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Ms.Staldues: 450-452, X',454,'X',456 <LIT>
A:Residues: 450-452, X',454,'X',456 <LIT>
R:Straczek, J: Maachl, F.; le Nguyen, D.; Becchi, M.; Heulin, M.H.; Nabet, P.; Bellevil
FEBS Lett. 373, 207-211, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Purification from human plasma of a tetrapeptide that potentiates insulin-like A;Reference number: $68059; MUID:96033974
A;Accession: $68059
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                                      A;Residues: 380-389 <KAT3>
R;Lenarcic, B.; Krasovec, M.; Ritonja, A.; Olafsson, I.; Turk, V.
FEBS Lett. 280, 211-215, 1991
A;Title: Inactivation of human cystatin C and kininogen by human cathepsin A;Reference number: S14303; MUID:91192133
A;Recession: S14447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Contents: annotation; gene organization R; Pierce, J.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein
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A; Molecule type:
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Best Local S:
Matches 12;
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N'Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen N'Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen N'Contains: bradykinin (kallidin); kininogen I; kininogen II; prokininogen C; Species: Bos primigenius taurus (cattle)
C; Date: 14 Nov-1981 #sequence_revision 14 Nov-1983 #text_change 22-Jun-1999
C; Accession: A01281; A91923; A91938; A29559
R; Kitamura, N.; Takagadaki, Y.; Furuto, S.; Tanaka, T.; Nawa, H.; Nawa, H.; Nakanishi, S.
R; Rittle: A single gene for bovine high molecular weight and low molecular weight kini A; Recession: A01281
A; Rocession: A01281
A; Rocession: A01281
A; Rocession: A01491; GB: K01757; NID: 9491; PIDN: CAA24735.1; PID: 9492
B; Rato, H.; Nagasawa, S.; Suzuki, T.
J; Biochem. 67, 313-223, 1970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Studies on the structure of bovine kininogen: cleavages of disulfide bonds a A;Reference number: A91923; MUID:70180420
A;Accession: A91923
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Pred. No. 4;
2; Mismatches
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Gaps

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A; Cross-references: GB:V00427; GB:J00011; NID:g489; PIDN:CAA23710.1; PID:g490
A; Cross-references: GB:V00427; GB:J00011; NID:g489; PIDN:CAA23710.1; PID:g490
C; Comment: The LMW kininogen proteinase inhibitor, takes part in initiation of C; Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator xyproline residue is present in the kininogen prior to the release of bradykinin.
C; Superfamily: kininogen; cystatin homology
C; Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; g; 1-18/Domain: signal sequence #status predicted <SIG>F; 19-434/Product: LMW kininogen II #status predicted <MAT>F; 19-434/Product: LMW kininogen II #status predicted <MAT>F; 19-130/Domain: cystatin homology <CXI>F; 19-130/Domain: cystatin homology <CXI>F; 141-252/Domain: cystatin homology <CXI>F; 151-37/Domain: cystatin homology <CXI>F; 151-37/Domain: cystatin homology <CXI>F; 151-386/Product: LWW kininogen II h#status predicted <BDX>F; 377-386/Product: Lysyl-bradykinin (kallidin II) #status syperimental <LCH>F; 38-386/Product: Lysyl-bradykinin (kallidin II) #status predicted <BDX>F; 377-386/Product: Lysyl-bradykinin (kallidin II) #status predicted <BDX>F; 377-386/Product: Lysyl-bradykinin (kallidin II) #status predicted <BDX>F; 377-386/Product: Lysyl-bradykinin (kallidin II) #status predicted SBJ / SBG/Product: Lysyl-bradykinin (kallikrein) #status predicted SBG/F; 386/Modified site: Pyrolidione carboxylic caid (Gln) (in mature form) #status predicted F; 386/Modified site: Arg-Ser (kallikrein) #status predicted SBG/Cleavage site: Arg-Ser (kallikrein) #status predicted
                                 R;Nawa, H.; Kitamura, N.; Hirose, T.; Asai, M.; Inayama, S.; Nakanishi, S. Proc. Natl. Acad. Sci. U.S.A. 80, 90-94, 1983
A;Title: Primary structures of bovine liver low molecular weight kininogen precursors
A;Reference number: A93984; MUID:83117859
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 01-Dec-2000
C;Accession: I56530; A39748; JH0454
R;Hawley, R.J.; Schelbe, R.J.; Wagner, J.A.
J. Nouroscl. 12, 2573-2581, 1992
A;Title: NGF induces the expression of the VGF gene through a cAMP or response elemen A;Reference number: I56530; MUID:92309005
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J. Neurochem. 57, 991-996, 1991
A;Title: Nucleotide sequence and regulatory studies of VGF, a nervous system-specific
A;Reference number: JH0454; MUID:91318308
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A; Residues: 1-617 RESS-
A; Cross-treferences: GB:M4223; NID:g207650; PIDN:AAA42336.1; PID:g207651
R; Salton, S.R.J.; Fischberg, D.J.; Dong, K.W.
Mol. cell. Biol. 11, 2335-2349, 1991
Mol. cell. Biol. 11, 2335-2349, 1991
A; Fitle: Structure of the gene encoding VGF, a nervous system-specific mRNA that is
A; Reference number: A39748; MUID:91203852
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Pred. No. 6.3;
1; Mismatches
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A;Residues: 1-175,'D',177-617 <SAL1>
A;Cross-references: GB:M60522
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A;Residues: 1-175,'D',177-617 <SAL2>
A;Cross-references: GB:M60525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68.38;
72.78;
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Best Local Similarity 72.7
Matches 8; Conservative
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                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-434 <NAW>
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                                                                                                                                                                                                              A; Accession: A01284
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                                                                                                                              A.Title: Studies on the primary structure of bovine high-molecular-weight kininogen. Amj A.Racession. A91938 MUID:75170265
A.Racession. A91938
A.R
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F;388-389/Cleavage site: Arg-Ser (Kallikrein) *status experimental
F;398-406,512/Rinding site: carbohydrate (Ser) (covalent) *status experimental
F;399,400,520,524,536,548,553,570/Rinding site: carbohydrate (Thr) (covalent) *status
F;498-499/Cleavage site: Arg-Thr (Kallikrein) *status experimental
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NyAlternate names: alpha-2-thiol proteinase inhibitor; preprokininogen
N'Convains: bradykinin (kallidin); kininogen I; kininogen II; prokininogen
N'Convains: Bos primigenius taurus (cattle)
C'Species: Bos primigenius taurus (cattle)
C'Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 28-May-1999
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Pred. No. 5.9;
2; Mismatches 1
A;Molecule type: protein
A;Residues: 378-393 «KAT»
R;Han, Y.N.; Komiya, M.; Iwanaga, S.; Suzuki, T.
J. Biochem. 77, 55-68, 1975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70.0%;
72.7%;
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281 LSHSIAKLNAE 291
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Best Local Similarity
Matches 8; Conserva
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189 TRTHTLTRVNLE 200
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Best Local Similarity
Matches 7; Conserv
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Best Local Similarity
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A;Note: article in Japanese
C;Comment: The HMW kininogen precursor is produced from the same gene as the LMW form as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: A single gene for bovine high molecular weight and low molecular weight kininog
A;Reference number: A93317; MUID:84014106
A;Accession: A01282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A) Molecule type: protein
A) Residues: 387-745 cHRA
A) Note: 398-700, 401-Val, and 455-Lys were also found
B; Han, Y.N.; Komiya, M.; Iwanaga, S.; Suzuki, T.
Blochem. 77, 55-68, 1975
A) Fitle: Studies on the primary structure of bovine high-molecular-weight kininogen. Ami A) Reference number: A91938; MUID:75170265
A;Experimental source: cultured cell PC12, clone NGF33.1
C;Comment: This protein is induced in PC12 cells to a greater extent by nerve growth faq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: The amino acid sequence of the light chain of human high-molecular-mass kininog A;Kefference number: Agl153; MUID:86030270
A;Contents: annotation; bovine cleavage sites; bovine carbohydrate binding sites R;Sueyoshi, T.; Miyata, T.; Kato, H.; Iwanaga, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R.Kato, H.; Nagasawa, S.; Suzuki, T.
T. Biochem. 67, 313-323, 1970
A.Fitle: Studies on the structure of bovine kininogen: cleavages of disulfide bonds and
A.Reference number: A91923; MUID:70180420
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A. Mesidues: 456-4696 (4Hz.)

R. Residues: 456-4696 (4Hz.)

R. Sueyoshi, T.: Miyata, T.; Hashimoto, N.; Kato, H.; Hayashida, H.; Miyata, T.; Iwanaga, J. Biol. Chem. 262, 2768-2779, 1987

J. Biol. Chem. 262, 2768-2779, 1987

A. Fittle: Bovine high molecular weight kininogen. The amino acid sequence, positions of characterise number: A92627; MUID:87137530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Residues: 376.391 <KAT>
R; Han, Y.N.; Kato, H.; Iwanga, S.; Suzuki, T.
J. Blochem. 79, 1201-1222, 1976
A; Title: Primary structure of bovine plasma high-molecular-weight kininogen. The amino
A; Reference number: A91941; MUID: 76260155
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A;Residues: '2',20-104,'E',106-256,'XX',257-376 <SUE>
R;Lottspeich, F.; Kellermann, J.; Henschen, A.; Foertsch, B.; Muller-Esterl, W.
Eur. J. Blochem. 152, 307-314, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Kitamura, N.; Takagaki, Y.; Furuto, S.; Tanaka, T.; Nawa, H.; Nakanishi, S.
Nature 305, 545-549, 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:V01492; GB:K01758; NID:9493; PIDN:CAA24736.1; PID:9494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NiAlternate names: alpha-2-thiol proteinase inhibitor; preprokininogen NiAlternate names: alpha-2-thiol proteinase inhibitor; preprokininogen NiContains: bradykinin (kallidin); kininogen I; kininogen II; prokininogen C; Species: Bos primigenius taurus (cattle)
C; Date: 14-Nov-1983 #sequence_revision 14 Nov-1983 #text_change 22-Jun-1999 C; Accession: A01282; A91923; A91941; A91938; B20559
                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                               Length 617;
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A;Title: Disulfide bonds in bovine HMW kininogens.
                                                                                                                                                                                                                           Score 41; DB 2;
Pred. No. 9.1;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               kininogen, HMW II precursor - bovine
                                                                                                                                                                                                                           68.3%;
58.3%;
                                                                                                                                                                                                                                                                                           Conservative
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190 TRTHTLTRVNLE 201
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                                                           C;Genetics:
A;Gene: VGF
C;Keywords: growth factor
                                                                                                                                                                                          Query Match
Best Local Similarity
'-hea 7; Conserv?
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A; Residues: 1-619 <KIT>
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C;Comment: Kininogen is a cysteine proteinase inhibitor, takes part in initiation of C;Comment: The glycine/histidine/lysine-rich region of HWW kininogen light chain is it C;Comment: Bradykinin, released from Kininogen by kallikrein, is a potent vasodilator xyproline residue is present in the Kininogen prior to the release of bradykinin.

C;Superfamily: kininogen; cystatin homology
C;Stperfamily: kininogen; cystatin homology
C;Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; d
F;118/Domain: signal sequence #status predicted <AMT>
F;118/Domain: cystatin homology <CXI>
F;19-130/Domain: cystatin homology <CXI
F;10-130/Domain: cystatin homology <CXI
F;10-130/Domain: cystatin homology <CXI
F;10-130/Domain: cystatin homology <CXI
F;10-130/Domain: cystatin 
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C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Date: 188.Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: F88.Aug-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C, Accession: S03381
R; Possenti, R.; Eldridge, J.D.; Paterson, B.M.; Grasso, A.; Levi, A.
EMBO J. 8, 2217-2223, 1989
A; Title: A protein induced by NGF in PC12 cells is stored in secretory vesicles and A; Reference number: S05381; MUID: 90005425
A; Accession: S05381
A; Status: not compared with conceptual translation
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C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 13-Nov-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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A; Residues: 1-711 <POS>
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-711/Product: VGF8a protein #status predicted <MAT>
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58.3%;
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VGF8a protein precursor - rat
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Gaps

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Indels

Length 90;

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C; Accession: Al0618
R; Parkhill, J; Dougan, G; James, K.D.; Thomson, N.R.; Pickard, D; Wain, J; Church th, T; Connerton, P; Croin, A.; Davis, P; Davies, R.M.; Dowd, L.; White, N.; Farr S; Moule S; O'Gaora, P.
Nature 413, 848-852, 2001
A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se A; Reference number: AB0502; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           conserved hypothetical bacteriophage protein STY1025 [imported] - Salmonella enterica Cispecies: Salmonella enterica subsp. enterica servoar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
                                                                                                                                                                                                                                         third complement component of axolotl
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A;Residues: 1-103 <FIG>
A;Cross-references: EMBL:AF001386; NID:g3294471; PIDN:AAC26074.1; PID:g3294485
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                                                    C;Species: Ambystoma mexicanum (axolot1)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 11-May-2000
C;Accession: A60526
R;Avila, D.; Lambris, J.D.
Comp. Biochem. Physiol. B 95, 839-845, 1990
A;Title: Isolation and characterization of the third complement component of A;Reference number: A60526; MUID:90263410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein 11 - Salmonella typhimurium
C;Species: Salmonella typhimurium
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                          A; Accession: A60526
A; Molecule type: protein
A; Residues: 1-90 <AVI>
C; Superfamily: alpha -2-macroglobulin
C; Keywords: complement pathway; cytolysis; glycoprotein; plasma
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Pred. No. 7.9;
2; Mismatches
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Pred. No. 6.8;
1; Mismatches
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submitted to the EMBL Data Library, June 1998
A;Reference number: 214818

    axolotl (fragments)

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ilarity 58.3%;
Conservative
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ilarity 63.6%;
Conservative
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44 TLAHTVEKRDAE 55
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Best Local Similarity
Matches 7; Conserv
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Best Local Similarity
Matches 7; Conserv
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A; Residues: 1-174 <PAR>
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                      complement C3
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Nature 406, 151-157, 2000

A; Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A; Note: Encare number: A82515; MUID:20365717

A; Note: for a complete list of authors see reference number A59328 below
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-534 cSIM>
A; Cross-references: GB:AEO04016; GB:AEO03849; NID:99107070; PIDN:AAF84770.1; GSPDB:GN001
A; Eschius: 1-534 cSIM>
A; Cross-references: GB:AEO04016; GB:AEO03849; NID:99107070; PIDN:AAF84770.1; GSPDB:GN001
A; Experimental source: strain 9a5c
B; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; B Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, E as-Nethors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Jonquela, M.L.; Kemper, B.L.; Kitajima, J.P.; Krieger, J.E.; Kuranee, E.E.; Laigr chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marcino, C.L.; Marques, M.V.; Martins, E.M.F.; Mateukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.P. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr. V. E.; de Sa, R.G.; Santelli, R.Y.; Santelli, R.J.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z. Chenters: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein YDR179w-a - yeast (Saccharomyces cerevisiae) (fragment)
N.Alternate names: hypothetical protein YD9395.13
C.Species: Saccharomyces cerevisiae
C.Date: 13-Jan-1995 #sequence_revision 10-Feb-1995 #text_change 29-Oct-1999
C.Accession: $49776; $51167
R.Murphy, L.; Harris, D.E.
Submitted to the EMBL Data Library, November 1994
A.Reference number: $49766
A.Reference number: $4976
A.Reference number: $4976
A.Residues: 1-498 CAUR>
A.Residues: 1-498 CAUR>
A.Residues: 1-498 CAUR>
A.Ross-references: EMBL:246727; NID:g1289283; PIDN:CAA86685.1; PID:e223726; PID:g128929
A.Rocession: $51167
A.Molecule type: DNA
A.Residues: 231-498 CAUW>
A.Residues: 231-49
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Pred. No. 27;
1; Mismatches
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Pred. No. 19;
1; Mismatches
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ilarity 58.3%;
Conservative
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8; Conservative
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359 TTAHAVAKLNAE 370
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nes 7; Conserv
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Best Local S
Matches 7
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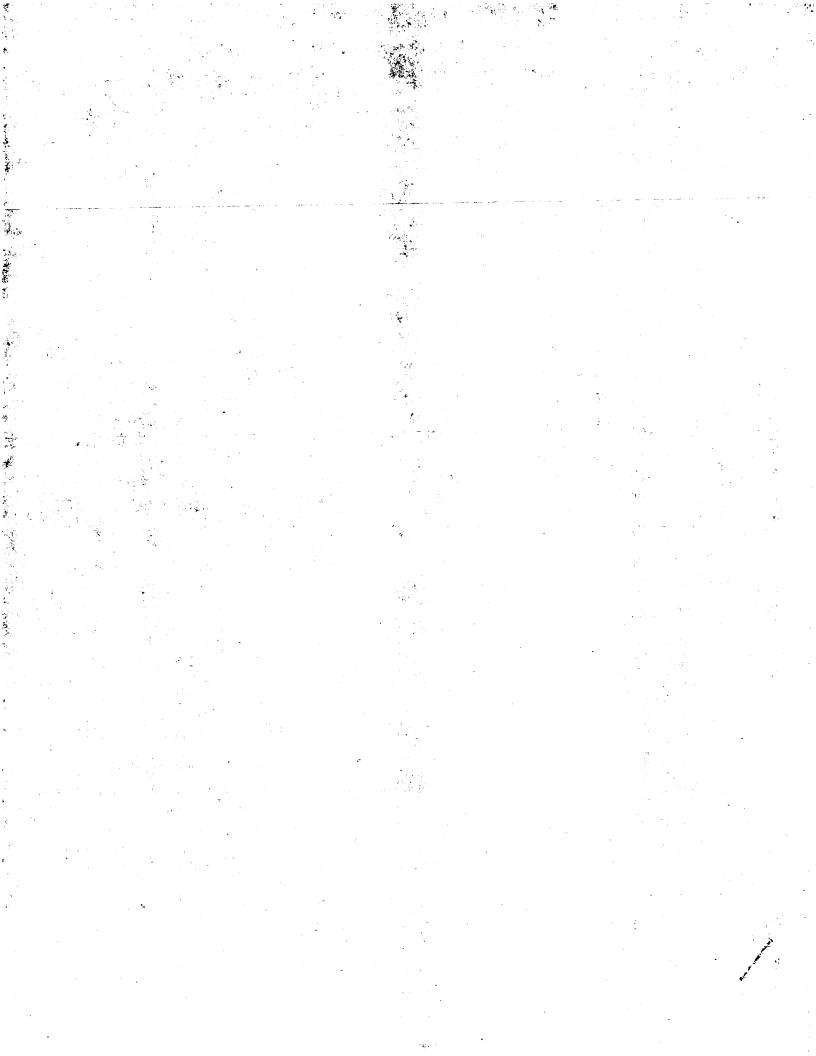
Gaps

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Length 103

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C; Superfamily: myosin heavy chain; myosin motor domain homology
C; Superfamily: myosin heavy chain; myosin motor domain homology
C; Superfamily: myosin heavy chain; mydrolase; methylated amino acid; muscle cc
F; 89-802/Domain: myosin motor domain homology <MMOT>
F; 202-209/Region: mucleotide-binding motif A (P-loop)
F; 690-712/Region: actin binding #status predicted
F; 793-807/Region: actin binding #status predicted
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A;Reference number: S02771; MUID:89178677
A;Accession: S02771
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A;Introns: 21/2; 115/2; 156/2; 247/3; 309/2; 376/3; 414/3; 585/3; 658/3; 734/2
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A; Residues: 1-1992 < WILL>
A; Residues: 1-1992 < WILL>
A; Cross-references: EMBL: 278199; PIDN: CABO1576.1; GSPDB: GN00023; CESP: KI2F2.1
A; Experimental source: clone K12F2
R; Dibb, N.J.; Maruyama, I.N.; Krause, M.; Karn, J.
J. Mol. Biol. 205, 603-613, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-786 <WIL>
A;Cross-references: EMBL:Z69794; PIDN:CAA93681.1; GSPDB:GN00028; CESP:R03G8.4
A;Experimental source: clone R03G8
                                                                                                                                                                                                                                                                                                C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T23883
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N:Contains: myosin ATPase (EC 3.6.1.32)
C;Species: Caenorhabditis elegans
C;Date: 31-Dec-1993 #sequence_revision 19-May-2000 #text_change 19-Jan-2001
C;Accession: T23622; S02771
                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 37; DB 2;
Pred. No. 68;
1; Mismatches
  Pred. No. 14;
2; Mismatches
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A;Molecule type: DNA
A;Residues: 1-116,140-1992 <DIB>
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63.68;
58.3%;
                              Conservative
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Best Local Similarity 63.6
Matches 7; Conservative
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A; Accession: T23622
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44 TLAHTVEKRDAE 55
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Best Local Similarity
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F;875-1992/Domain: coiled coil #status predicted <COI>
F;875-1893/Region: 12
F;1190-1992/Region: 119th meromyosin
F;1153/Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted
F;208/Binding site: ATP (Lys) #status predicted
F;208/Binding site: ATP (Lys) #status predicted
F;730,740/Active site: Cys #status predicted
F;730,740/Active site: Cys #status predicted
F;730,740/Active site: Cys #status predicted
F;730,740/Active site: ATP (Lys) #status predicted
F;730,740/Active site: Cys #status predicted
F;73
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                              OM protein - protein search, using sw model
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July 1, 2002, 16:30:12; Search time 21.51 Seconds (without alignments) 21.601 Million cell updates/sec

US-09-461-061A-3 56 1 IDNVKKARVQVV 12 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

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Q04217 saccharomyc Q24490 manduca sex Q10960 mycobacteri Q96095 lactococus Q92111 rattus norv Q95471 homo sapien Q95409 tickettsia Q56362 thiocapsa r P39942 bos taurus Q9558 homo sapien P57746 mus musculu Q97755 oryctolagus	644 AA. update) on update) proteinase inhibitor) (Contains:	aniata; Vertebrata; Euteleostomi; (tarrhini; Hominidae; Homo. 1 AND LMW).  Shi S.; for human high molecular of convas for human high molecular of for human high molecular high high molecular high molecular high molecular high molecular hi	ima D., Takagaki Y., Miyata T., human kininogen gene and a model for 5). T., Shiokawa H., Sasaki M.; lipha 2-thiol proteinase inhibitor and weight kininogen.";	A., Foertsch B., chain of human high-molecular- and kininogens."; ga S.; ens.";
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1267 13305 112 119 219 247 247 247	ARD; , Crea , Last , Last	ens (Human).  ens (Human).  Eutheria; Chordata  D=9606;  FROM N.A. (ISOFORMS  Ver;  5234582; PubMed=298  Y., Kitamura N., Na and sequence analys d low molecular weil.  Prekininogens.";  Chem. 260:8601-8609	Kitagawa H. Kitagawa H. Kitagawa H. Cyganization nn. ", 260:8610-9 1-401 FROM N 22621; PubMed turachi K., T turachi Low mo	); PubMed ellermann: sequence ; 152:307 389. ; PubMed ures of pures of pure
н м	STANDARD; 1. 01, Cr 1. 33, La 1. 40, La rsor (Alp	(Human) tazoa; (heria; ) 06; N.A. (; S82; Pul Kitamura sequence w molecy kininoga	Puh gawe izat 0:8( 0:8K Puh i K numan	Pub ller ller eque eque 152: 89. Pub res 57(1
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	LT 1  KNG_HUMAN STAND; PO1042; P01043; 21-JUL-1986 (Rel. 01 01-PEB-1996 (Rel. 33 16-OCT-2001 (Rel. 40 Kininogen precursor Bradykinin].	KNG. Homo sapiens (Human). Homo sapiens (Human). Eukaryota; Metazoa; Cho Mammalia; Eutheria; Pri NCBL_TaxID-9606; [1] SEQUENCE FROM N.A. (ISO) TISSUE-Liver; MEDLINE-85234582; PubMe Takagaki Y., Kitamura N "Cloning and sequence a weight and low molecula, two human prekininogens J. Biol. Chem. 260:8601 [2]	S STRU INE=8 amura anishi cuctur evolu siol. JENCE INE=8 IDO I. olatic ident	NE=866 NE=866 er-Es amino kininc kininc J. Bid NE=90 Ctura Proc.
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C. -!- FUNCTION: (1) KININOGENS ARE INHIBITORS OF THIOL PROTEASES; (2)
HWA-KININOGEN PLAYS AN IMPORTANT ROLE IN BLOOD COAGULATION BY '
HELPING TO POSITION OPTIMALLY PREKALLIKREIN AND FACTOR XI NEXT TO
FACTOR XII; (3) HWM-KININOGEN INHIBITS THE THROMEN-AND PLASMIN-
INDUCED AGGREGATION OF THROMBOCYTES; (4) THE ACTIVE PEPTIDE
BRADKININ THAT IS RELEASED FROM HWW-KININOGEN SHOWS A VARIETY OF
PHYSIOLOGICAL EFPECTS: (4A) INFLUENCE IN SMOOTH MUSCLE
CONTRACTION, (4B) INDUCTION OF HYPOTENSION, (4C) NATRIURESIS AND
DIURESIS, (4D) DECREASE IN BLOOD GLUCOSE LEVEL, (4E) IT IS A
MEDIATOR OF INFLAMMATION OF NOCICEPTORS (4E3) RELEASE OF
COTHER MEDIATORS OF INFLAMMATION (E.G. PROSTAGLANDINS), (4F) IT HAS
CARDIOPROFERIYE FEFECT (DIRECTLY UNDERLY) FACTON, (5)
LMW-KININOGEN INHIBITS THE AGGREGATION OF THROMBOCYTES, (6) LMW-
COTTOR THE CONTRAST TO HMM-KININOGEN NOT INVOLVED IN BLOOD
                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00287; CYSTATIN; 2.
Glycoprotein; Plasma; Repeat; Thiol protease inhibitor; Vasodilator;
Bradykinin; Blood coagulation; Inflammatory response; Signal;
                                                                                                                                                                                                                                      TISSUE SPECIFICITY: PLASMA.
PTM: BRADYKININ IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN.
SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
                                                                                                                                                                                                                  ALTERNATIVE PRODUCTS: 2 ISOFORMS; HWW (SHOWN HERE) AND LMW; ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                      SUBCELLULAR LOCATION: Secreted. ALTERNATIVE PRODUCTS: 2 ISOFORM
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PRINTS; PR00334; KININOGEN.
ProDom; PD001231; Cystatin_C_M; 1.
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InterPro; IPR003243; Cystatin_C_M.
InterPro; IPR002395; Kininogen.
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AAB59550.1; JOINED.
AAB59550.1; JOINED.
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MIM; 228960; -.
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AAB59551.1;
AAB59551.1;
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EMBL; MI1525; AAB5955
EMBL; MI1526; AAB5955
EMBL; MI1527; AAB59551
EMBL; MI1527; AAB59551
EMBL; MI1528; AAB59551
PIR; A01279; KQUUHI
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PIR; B25276; B25276.
PIR; S02482; S02482.
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M11525;
M11526;
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M11522;
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M11528;
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MEDLINE-83117859; PubMed-6572010;
Nawa H., Kitamura N., Hirose T., Asai M., Inayama S., Nakanishi S.;
"Primary structures of bovine liver low molecular weight kininogen precursors and their two mRNAs.";
Proc. Natl. Acad. Sci. U.S.A. 80:90-94(1983).
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20-0047,
21-UUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUMAR-2002 (Rel. 41, Last annotation update)
Kininogen, LMW II precursor (Thiol proteinase inhibitor) [Contains: Bradykinin].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos. NCBI_TaxID=9913;
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                                                                               KININGGEN LIGHT CHAIN.
CYSTATIN-LIKE 1.
CYSTATIN-LIKE 2.
CYSTATIN-LIKE 2.
HIS-RICH (ASSOCIATED WITH CLOTTING
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MISSING (IN ISOFORM LAW).
T -> I (IN REF. 1).
313284CBAF8FBB7E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                             PYRROLIDONE CARBOXYLIC ACID. INTERCHAIN.
                       KININGEN HEAVY CHAIN.
BRADYKININ.
                                                                                                                                                                                                                                                  ACTIVITY).
KININOGEN
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593
644 AA;
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Gaps

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Mismatches

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10; Conservative

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Matches
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                                                                                                    J. BIOL. Chem. 262:2768-2779(1987).

-!- FUNCTION: (1) KININOGENS ARE INHIBITORS OF THIOL PROTEASES; (2)

-LAW-KININOGEN INHIBITS THE AGGREGATION OF THROMBOCYTES; (3) THE
ACTIVE PEPTIDE KALLIDIN THAT IS RELEASED FROM LAW-KININOGEN SHOWS
A VAREETY OF PHYSIOLOGICAL EFFECTS: (3A) INFLUENCE IN SMOOTH
MUSCLE CONTRACTION, (3B) INDUCTION OF HYPOTENSION, (3C)

NATRIORESIS AND DIURESIS (KIDDEY).

-!- SUBCELJULAR LOCATION: Extracellular.

-!- SUBCELJULAR PRODUCTS: HWW II AND LAW II KININOGEN PRECURSORS ARE
PRODUCED FROM THE SAME GENE AS THE RESULT OF ALTERNATIVE MINA
SPLICING. THE SEQUENCES OF BOTH KININOGENS ARE IDENTICAL UP
                                                                                                                                                                                                                                                                                                              -i- PTM: BRADYKININ IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN.
-i- MISCELLANEOUS: LAW-KININOGEN IS IN CONTRAST TO HWW-KININOGEN NOT
INVOLVED IN BLOOD CLOTTING.
                                            Miyata T., Iwanaga S.;
"Bovine high molecular weight kininogen. The amino acid sequence,
positions of carbohydrate chains and disulfide bridges in the heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00287; CYSTATIN, 2.
Glycoprotein; Plasma; Repeat; Vasodilator; Alternative splicing;
Thiol protease inhibitor; Bradykinin; Signal,
SIGNAL 1 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .); OR 169.
.) (PARTIAL).
                             Sueyoshi T., Miyata T., Hashimoto N., Kato H., Hayashida H.,
Miyata T., Iwanaga S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HEAVY CHAIN.
BRADYKININ.
LIGHT CHAIN.
CYSTATIN-LIKE 1.
CYSTATIN-LIKE 2.
CYSTATIN-LIKE 3.
PYRROLIDONE CARBOXYLIC ACID.
N-LINKED (GLCNAC. .), OR 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48148 MW; 73A7079DE3E03430 CRC64;
                                                                                                                                                                                                                                                                                                                                                              -1- SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KININOGEN, LAW II
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InterPro; IPR000010; Cystatin.
InterPro; IPR003243; Cystatin.C.M.
Pfam; PF00031; Cystatin.C.M.
ProDom; PD001231; Cystatin.C.M; 1.
             MEDLINE-87137530; PubMed-3546295;
                                                                                                                                                                                                                                                                                                 -1- TISSUE SPECIFICITY: PLASMA.
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434 AA;
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Score 44; DB 1; Length 434; Pred. No. 0.8;

78.6%; 83.3%;

Best Local Similarity

Query Match

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J. Biol. Chem. 263:2768-2779(1987).
J. Biol. Chem. 263:2768-2779(1987).
J. FUNCTION: (1) KININOGENS ARE INHIBITORS OF THIOL PROTEASES; (2)
LAM-KININOGEN INHIBITS THE AGGREGATION OF THROMBOCYTES; (3) THE
ACTIVE PEPTIDE KALLIDIN THAT IS RELEASED FROM LAM-KININOGEN SHOWS
A VARIETY OF PHYSIOLOGICAL EFFECTS: (3A) INFLUENCE IN SMOOTH
MUSCLE CONTRACTION, (3B) INDUCTION OF HYPOTENSION, (3C)
NATRIURESIS AND DIURESIS (KIDNEY).
I- SUBCELLULAR LOCATION: EXTERCELLULAR.
PRODUCED FROM THE SAME GENE AS THE RESULT OF ALTERNATE MRNA
SPLICING: THE SEQUENCES OF BOTH KININOGENS ARE IDENTICAL UP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE SPECIFICITY: PLASMA.
PTM: BRADYKININ IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN.
MISCELLANEOUS: LMW-KININOGEN IS IN CONTRAST TO HMW-KININOGEN NOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 19-378.
MEDLINE-87137530; PubMed-3546295;
Sueyoshi T., Miyata T., Hashimoto N., Kato H., Hayashida H.,
Miyata T., Iwanaga S.;
"Bovine high molecular weight kininogen. The amino acid sequence,
positions of carbohydrate chains and disulfide bridges in the heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-83117859; PubMed-6572010;
MEDLINE-83117859; Nakanishi S.;
Nawa H., Kitamura N., Hirose T., Asai M., Inayama S., Nakanishi S.;
"Primary structures of bovine liver low molecular weight kininogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Kininogen, LMW I precursor (Thiol proteinase inhibitor) [Contains:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00287; CYSTATIN; 2.
Glycoprotein; Plasma; Repeat; Vasodilator; Alternative splicing;
Thiol protease inhibitor; Bradykinin; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INVOLVED IN BLOOD CLOTTING.
SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               precursors and their two mRNAs.";
Proc. Natl. Acad. Sci. U.S.A. 80:90-94(1983).
                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000010; Cystatin.
InterPro; IPR003243; Cystatin_C_M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00031; cystatin; 3.
ProDom; PD001231; Cystatin_C_M; 1.
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PIR; A01283; KGBOL1.
                                                                                                                                                                                                                                             STANDARD;
                                                               298 IDTVKKATVQVV 309
1 IDNVKKARVQVV 12
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ID KNL1_BOVIN
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                                                                                                                                                                                                                                                                                                                                                                                                     Kitamura N., Takagaki Y., Furuto's., Tanaka T., Nawa H., Nakanishi S.; "A single gene for bovine high molecular weight and low molecular weight kininogens.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 376-391.
MEDLINE-70180420; PubMed=4986212;
Kato H., Nagasawa S., Suzuki T.;
"Studies on the structure of bovine kininogen: cleavages of disulfide bonds and of methionyl bonds in Kininogen-II.";
J. Biochem. 67:313-323(1970).
                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Kininogen, HMW II precursor (Thiol proteinase inhibitor) (Contains:
                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos. MCBI_TaxID=9913;
                                                                                                                                                                                                                        ;;
                                                                 N-LINKED (GLCNAC. .).
O-LINKED (GLCNAC. .).
O-LINKED (CLCNAC. .); OR 169.
N-LINKED (GLCNAC. .), (PARTIAL).
N-LINKED (GLCNAC. .).
                                                                                                                                                                           A -> T (IN REF. 1; CAA23709).
F01F7EB6814BCE6C CRC64;
                                                                                                                                                                                                       Score 44; DB 1; Length 436;
Pred. No. 0.8;
                                                            PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                        2; Indels
        KININOGEN, LMW I.
                                    CYSTATIN-LIKE 1.
CYSTATIN-LIKE 2.
CYSTATIN-LIKE 3.
                                                                                                                                                                                                                        0; Mismatches
               HEAVY CHAIN.
BRADYKININ.
                              LIGHT CHAIN.
                                                                                                         INTERCHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chain portion.";
J. Biol. Chem. 262:2768-2779(1987).
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-84014106; Pubmed-6571699;
                                                                                                                                                                                  48427 MW;
                                                                                                                                                                                                         78.68;
                                                                                                                                                                                                               83.3%;
                                                                                                                                                                                                       Query Match
Best Local Similarity 83.3
Matches 10; Conservative
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SEQUENCE OF 19-376.
                                                                                                                                                                                                                                                                                                                                      Bradykinin]
                                                                                                                                                                                                                                                                                 KNH2_BOVIN
ID KNH2_BOVIN
                                                  DOMAIN
MOD_RES
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 456-496.

MEDLINE=75170265; PubMed=1169237;

A Han Y.N., Komiya M., Iwanaga S., Suzuki T.;

A Han Y.N., Komiya M., Iwanaga S., Suzuki T.;

A thinogen. Amino acid sequence of a fragment ('histidine-rich peptide') released by plasma kallikrein.";

I peptide') released by plasma kallikrein.";

J. Blochem. 77:55-68(1975)

C --- FUNCTION: (1) KININOGENS ARE INHIBITORS OF THIOL PROTEASES; (2) HWW-KININOGEN PLAYS AN IMPORTANT ROLE IN BLODD COAGULATION BY HELPING TO POSITION OPTIMALLY PREKALLIKREIN AND FACTOR XI NEXT TO FACTOR XII; (3) HWW-KININOGEN INHIBITS THE THROMBIN- AND PLASMIN-INDUCED AGGREGATION OF THROMBOCYTES; (4) THE ACTIVE PEPTIDE BRADYKININ THAT IS RELEASED FROM HWW-KININOGEN SHOWS A VARIETY OF PHYSIOLOGICAL BFFECTS: (4A) INFLUENCE IN SMOOTH WUSCLE CONTRACTION, (4B) INDUCTION OF HYPOTENSION, (4C)

NATRIURESIS AND DIURESIS, (4D) DECREASE IN BLOOD GLUCOSE LEVEL, (4E) IT IS A MEDIATOR OF INFLAMMATION AND CAUSES (4E1) INCREASE IN VASCULAR PERWEABILITY, (4E2) STIMULATION OF NOCICEPTORS (4E3) RELEASE OF OTHER MEDIATORS OF INPLAMMATION (E.G. PROSTAGLANDINS), (4F) IT HAS A CARRIDORPOTENTY BEPECTIV VIA BRADYKININ CHANNO CHANNO FOLDER ACTION, INDIRECTLY VIA BRADYKININ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELTULAR LOCATION: EXTRACEILULAR.
-!- ALTERNATIVE PRODUCTS: HWW II AND LAW II KININOGEN PRECURSORS ARE PRODUCED FROM THE SAME GENE AS THE RESULT OF ALTERNATE MRNA SPLICING. THE SEQUENCES OF BOTH KININOGENS ARE IDENTICAL UP
                              MEDIINE-6260155; PubMed-956151;
Han Y.N., Kato H., Iwanaga S., Suzuki T.;
"Primary structure of bovine plasma high-molecular-weight kininogen."
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-!- SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
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                                                                                                                                                                                                              The amino acid sequence of a glycopeptide portion (fragment 1) following the C-terminus ot the bradykinin moiety.";
J. Biochem. 79:1201-1222(1976).
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BRADYKININ.
LIGHT CHAIN.
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PIR; B29559; B29559.
InterPro; IPR000010; Cystatin.
InterPro; IPR000343; Cystatin.
InterPro; IPR003543; Cystatin.
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EMBL; V01492; CAA24737.1; ALT_SEQ.
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SEQUENCE OF 387-455.
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                                                                              TO FACTOR XII; (3) HWW-KININGEN INTELLED AND FACION AT INCAPABLY FACTOR XII; (3) HWW-KININGEN INTELLED AND FACION AT INCAPABLY FACTOR XII; (3) HWW-KININGEN INTELLED FOR THE ACTIVE PETITIOE BRADYKININ THAT IS RELEASED FROM HWW-KININGEN SHOWS A VARIETY OF PHYSIOLOGICAL EFFECTS: (4A) INFLUENCE IN SWOOTH MUSCLE CONTRACTION, (4B) INDUCTION OF HYPOTESSION, (4C) MATICIPESIS AND DIURESIS, (4D) DECREASE IN BLOOD GLUCOSE LEVEL, (4E) IT IS A MEDIATOR OF INFLAMMATION AND CAUSES (4E1) INCREASE IN VASCULAR PERMEABILITY, (4E2) STIMULATION OF NOCICEPTORS (4E3) RELEASE OF OTHER MEDIATORS OF INFLAMMATION (5.C. PROSTAGLANDINS) ACTION, INDIRECTLY VIA ENDOTHELIUM-DERIVED RELEAST
                                                                                                                                                                                                                                                                                                                           TISSUE SPECIFICITY: PLASMA.
PTM: BRADYKININ IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN.
SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
                                                                                                                                                                                                                                                     SUBCELÍULAR LOCATION: Extracellular.
ALTERNATIVE PRODUCTS: HWW I AND LAW I KININOGEN PRECURSORS ARE PRODUCED FROM THE SAME GENE AS THE RESULT OF ALTERNATE MINA SPLICING. THE SEQUENCES OF BOTH KININOGENS ARE IDENTICAL UP
                                          FUNCTION: (1) KININOGENS ARE INHIBITORS OF THIOL PROTEASES; (2) HMW-KININOGEN PLAYS AN IMPORTANT ROLE IN BLOOD COAGULATION BY HELPING TO POSITION OPTIMALLY PREKALLIRREIN AND FACTOR XI NEXT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pfam; PF00031; cystatin; 3.
PRINTS; PR00334; KININGEN.
PRODOM: PD001231; Cystatin_C_M; 1.
SMART; SM00043; CY; 3.
PROSITE; PS00287; CYSTATIN; 2.
PROSITE; PS00287; CYSTATIN; 2.
Tycoprotein; Plasma; Repeat; Vasodilator; Alternative splicing; Thiol protease inhibitor; Bradykinin; Blood coagulation; Inflammatory response; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. .); OR 169.
N-LINKED (GLCNAC. .) (PARTIAL).
N-LINKED (GLCNAC. .)
kininogen. Amino acid sequence of a fragment ('histidine-rich
peptide') released by plasma kallikrein.";
J. Biochem. 77:55-68(1975).
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BRADYKININ.
LIGHT CHAIN.
CYSTATIN-LIKE 1.
CYSTATIN-LIKE 2.
CYSTATIN-LIKE 3.
PYROLIDONE CARBOXYLIC ACID.
N-LINKED (GLCNAC. . .).
O-LINKED (GLCNAC. . .).
N-LINKED (GLCNAC. . .).
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PIR; A29559; A29559.
InterPro; IPR000010; Cystatin.
InterPro; IPR003243; Cystatin.C.M.
InterPro; IPR002395; Kininogen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDINE-7019/01/2019 Pubmed-4986212;
Kato H., Nagasawa S., Suzuki T.;
"Studies on the structure of bovine kininogen: cleavages of disulfide bonds and of methionyl bonds in kininogen-II.";
J. Biochem. 67:313-323(1970).
                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 19-378.
MEDLINE-87137530; PubMed-3546295;
Sueyoshi T., Miyata T., Hashimoto N., Kato H., Hayashida H.,
Miyata T., Iwanaga S.;
"Bovine high molecular weight kininogen. The amino acid sequence,
positions of carbohydrate chains and disulfide bridges in the heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus (Bovine).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria: Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinne; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Last sequence update)
1-Jul-1980 (Rel. 41, Last annotation update)
Klninogen, HMW I precursor (Thiol proteinase inhibitor) (Contains:
Bradyklnin].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-84014106; PubMed-6571699;
Kitamura N., Takagaki Y., Furuto S., Tanaka T., Nawa H., Nakanishi
"A single gene for bovine high molecular weight and low molecular
weight kininogens.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 458-498.
MEDLINE-75170265; PubMed-1169237;
Han Y.N., Komiya M., Iwanaga S., Suzuki T.;
"Studies on the primary structure of bovine high-molecular-weight
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                                             (PARTIAL)
              (PARTIAL).
(GLCNAC. ..); OR 169.
(GLCNAC. ..) (PARTIAI
                                                                                                                                                                                                                                                                                                              Length 619;
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H -> K.
H +> P04320A8EB0EE0DA CRC64;
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Pred. No. 1.1;
0; Mismatches
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83.3%;
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Best Local Similarity 83.3
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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298 IDTVKKATVQVV 309
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SEQUENCE FROM N.A.
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KNH1_BOVIN
ID KNH1_BOVIN
AC P01044;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDILINE-81250580; PubMed-2139509;
MEDILINE-81250580; PubMed-2139509;
Fung W.-P., Schreiber G.;
Structure and expression of the genes for major acute phase alpha 1-
protein (thiostatin) and kininogen in the rat.";
J. Biol. Chem. 262:9298-9308(1987).
-!- FUNCTION: KININOGENS ARE PLASMA GLYCOPROTEINS WITH A NUMBER OF
FUNCTION: (1) AS PRECURSOR OF THE ACTIVE PEPTIDE BRADXKININ THEY
BEFECT SMOOTH WISCLE CONTRACTION, INDUCTION OF HYOPIENSION AND
INCREASE OF VASCULAR PERMEABILITY. (2) THEY PLAY A ROLE IN BLOOD
COAGULATION BY HELPING TO POSITION OPTIMALLY PREKALLIKREIN AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cole T., Inglis A.S., Roxburgh C.M., Howlett G.J., Schreiber G.; "Major acute phase alpha 1-protein of the rat is homologous to bovine kiningen and contains the sequence for bradykinin: its synthesis is regulated at the mRNA level."; FEBS Lett. 182:57-61(1985).
                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTM: AS T-KININ IS PRECEDED BY A MET INSTEAD OF AN ARG OR LYS, IT IS NOT RELEASED FROM ITS PRECURSOR BY EITHER TISSUE OR PLASMA
                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE SPECIFICITY: PLASMA.
INDUCTION: IN RESPONSE TO AN INFLAMMATORY STIMULANT. T-KININOGEN
II SYNTHESIS IS INDUCED AND THE PLASMA CONCENTRATION OF
T-KININOGEN I IS RAISED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Furuto-Kato S., Matsumoto A., Kitamura N., Nakanishi S.; "Primary structures of the mRNAs encoding the rat precursors for bradykinin and T-kinin. Structural relationship of kininogens with major acute phase protein and alpha 1-cysteine proteinase inhibitor.":
                                                                                                                                                                                                       KW71_RAT STANDARD; PRT; 430 AA.
P01048; P04081;
01-NOV-1986 (Rel. 03, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
01-NAR-2002 (Rel. 41, Last annotation update)
T-kininogen I precursor (Major acute phase protein) (Alpha-1-MAP)
(Thiostatin) [Contains: T-kinin].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FACTOR XI NEXT TO FACTOR XII. (3) THEY ARE INHIBITOR OF THIOL
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MEDILPS-86008256; PubMed-4413019;
Anderson K.P., Heath E.C.;
"The relationship between rat major acute phase protein and the
                                         ö
Score 44; DB 1; Length 621;
Pred. No. 1.1;
); Mismatches 2; Indels
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MEDLINE=86008264; Pubmed=2413018;
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MEDLINE-85127561; PubMed-2578992;
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 78.6%;
83.3%;
                                         Conservative
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                     Similarity
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                          TABLE, REF.2. SEQUENCE DIFFERS FROM THAT SHOWN IN POSITIONS: 257, 262,269,295,314,315,331,332, AND 389. IN ALL THOSE POSITIONS THE ALTERNATE AMINO-ACID IS THE ONE PRESENT IN T-II KININOGEN.
SAME GENE, AND TWO ADDITIONAL LAW-LIKE KININGENS: T-I AND T-II.
-!- SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
-!- CAUTION: IN ADDITION TO THE CONFLICTS DESCRIBED IN THE FEATURE
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Glycoprotein; Plasma; Repeat; Vasodilator; Multigene family;
Thiol protease inhibitor; Bradykinin; Acute phase; Signal.
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BY SIMILARITY.

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C -> Y (IN REF. 3).
C -> Y (IN REF. 3).
S -> F (IN REF. 2 AND 3).
REV -> TKI (IN REF. 2).
N -> D (IN REF. 2).
R -> F (IN REF. 2).
T -> R (IN REF. 2).
T -> R (IN REF. 2).
T -> X (IN REF. 2).
H -> Y (IN REF. 2).
H -> Y (IN REF. 2).
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CYSTATIN-LIKE 1.
CYSTATIN-LIKE 2.
CYSTATIN-LIKE 3.
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EMBL; M1642; AAA41568.1; --
EMBL; X02299; CAA26162.1; ALT_SEQ.
PIR; A01286; KGRTT1.
PIR; A01287; KGRTM.
PIR; A23897; A23897.
PIR; A27115; A27115.
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InterPro; IPR000010; Cystatin.
InterPro; IPR003243; Cystatin_C_M.
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ProDom; PD001231; Cystatin_C_M; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. BLOL. Chem. 260:12054-12059(1985).

-1. FUNCTION: KININGGENS ARE PLASMA GLYCOPROTEINS WITH A NUMBER OF FUNCTION: (1) AS PRECURSOR OF THE ACTIVE PEPTIDE BRADYKININ THEY EFFECT SMOOTH MUSCLE CONTRACTION, INDUCTION OF HYPOTENSION AND INCREASE OF VASCULAR PERREABILITY. (2) THEY PLAY A ROLE IN BLOOD COAGULATION BY HELPING TO POSITION OPTIMALLY PREKALLIKREIN AND FACTOR XI NEXT TO FACTOR XII. (3) THEY ARE INHIBITOR OF THIOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T-KININGEN I IS RAISED.
PTM: AS T-KININ IS PRECEDED BY A MET INSTEAD OF AN ARG OR LYS, IT
IS NOT RELEASED FROM ITS PRECURSOR BY EITHER TISSUE OR PLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Extracellular.
-!- TISSUE SPECIFICITY: PLASMA.
-!- INDUCTION: IN RESPONSE TO AN INFLAMMATORY STIMULANT. T-KININGEN
II SYNTHESIS IS INDUCED AND THE PLASMA CONCENTRATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HMW AND LAW KININOGENS PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE, AND TWO ADDITIONAL LAW-LIKE KININOGENS: T-I AND T-II. SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Furuto-Kato S., Matsumoto A., Kitamura N., Nakanishi S.;
"Primary structures of the mRNAs encoding the rat precursors for bradykinin and T-kinin. Structural relationship of kininogens with major acute phase protein and alpha 1-cysteine proteinase inhibitor.";
                                                                                                                                                                                                                                                                                                                   01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
T-Kininogen II precursor (Major acute phase protein) (Alpha-1-MAP)
(Thiostatin) [Contains: T-Kinin].
                                                                                                                                              ;
                                                                                                               Score 38; DB 1; Length 430;
                                                                                                                                              Indels
R -> G (IN REF. 2 AND 3).
A -> L (IN REF. 2).
DH -> ER (IN REF. 3).
P -> S (IN REF. 1).
N; FAEBB78FAF4723C3 CRC64;
                                                                                                                                                                                                                                                                                       430 AA
                                                                                                                                             Mismatches
                                                                                                                              Pred. No.
                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlycosultebB: P08932; --
GlycosultebB: P08932; --
InterPro; IPR000010; Cystatin.
InterPro; IPR003243; Cystatin_C_M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00031; cystatin; 3.
ProDom; PD001231; Cystatin_C_M; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-86008264; PubMed-2413018;
                                                                 Ψ
                                                                                                            67.9%;
75.0%;
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                                                                47715
                                                                                                                                             9; Conservative
                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
                                                                                                                                                                                            300 IDTVKKATSQVV 311
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 414
415
420
430
430 AA;
                                                                                                            Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KALLIKREIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEASES
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P08932;
CONFLICT
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fung W.-P., Schreiber G.; "Structure and expression of the genes for major acute phase alpha 1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Furuto-Kato S., Matsumoto A., Kitamura N., Nakanishi S.; "Primary structures of the mRNAs encoding the rat precursors for bradykinin and T-kinin. Structural relationship of kininogens with major acute phase protein and alpha 1-cysteine proteinase inhibitor ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kitagawa H., Kitamura N., Hayashida H., Miyata T., Nakanishi S.; "Differing expression patterns and evolution of the rat kininogen
                                                                                                                                                                                                                                                                                                                                         . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
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          PROSITE; PS00287; CYSTATIN; 2.
Glycoprotein; Plasma; Repeat; Vasodilator; Multigene family;
Thiol protease inhibitor; Bradykinin; Acute phase; Signal.
                                                                                                                                                                        INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
CONTRAINED (GLONAC. .) (POTENTY.
N-LINKED (GLONAC. .) (POTENTY.)
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10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                        43EDF02D1BF55076 CRC64;
                                                                                                                             CYSTATIN-LIKE 1.
CYSTATIN-LIKE 2.
CYSTATIN-LIKE 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1988 (Rel. 09, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Kininogen precursor [Contains: Bradykinin].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       639 AA
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MEDLINE-87137443; Pubmed-3029068;
                                                                                       CHAIN.
                                                                                                                     LIGHT CHAIN.
                                                                         KININOGEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biol. Chem. 260:12054-12059(1985).
                                                                                                    T-KININ-T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene family.";
J. Biol. Chem. 262:2190-2198(1987).
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MEDLINE-86008264; PubMed-2413018;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   p08934; p08933;
01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last section)
16-OCT-2001 (Rel. 40, Last and
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75.08;
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SMART; SM00043; CY; 3.
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205
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430 AA;
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Best Local Similarity
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- PTM: BRADYKININ IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN.
-!- MISCELLANEOUS: RAT EXPRESS FOUR TYPES OF KININOGENS: THE CLASSICAL HMW/LMW KININOGENS AND TWO ADDITIONAL LMW-LIKE KININOGENS: T-I AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00043; CY; 3.
PROSITE; PS00287; CYSTATIN; 2.
Glycoprotein; Plasma; Repeat; Thiol protease inhibitor; Vasodilator;
Bradykinin; Blood coagulation; Inflammatory response; Signal;
Alternative splicing; Multigene family.
SIGNAL
1 18
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-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; HWW (SHOWN HERE) AND LMW; ARE PRODUCED BY ALTERNATIVE SPLICING.
-1- TISSUE SPECIFICITY: PLASMA.
                                                                                                                                                                                               transcription initiation sites
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KININOGEN LIGHT CHAIN.
CYSTATIN-LIKE 1.
CYSTATIN-LIKE 2.
CYSTATIN-LIKE 3.
HIS-RICH.
                                                                                                             STRAIN=WISTAR; TISSUE-Liver;
BELLINE=87187465; BUDMed=3818598;
Kageyama R., Fitamura N., Ohkubo H., Nakanishi S.;
"Differing utilization of homologous transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KININOGEN.
KININOGEN HEAVY CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
protein (thiostatin) and kininogen in the rat."; J. Biol. Chem. 262:9298-9308(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L29428; AAA41486.1; -.
EMBL; M11884; AAA41487.1; -.
EMBL; M14369; AAA41484.1; -.
EMBL; M14369; AAA41485.1; ALT_SEO.
EMBL; M16455; AAA41482.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P01040; 1DVD.
InterPro; IPR000010; Cystatin.
InterPro; IPR003243; Cystatin_C_M.
InterPro; IPR002395; Kininogen.
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ProDom; PD001231; Cystatin_C_M; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00031; cystatin; 3.
                                                                                  OF 1-41 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A25486; A25486.
PIR; A28055; A28055.
                                                                                     SEQUENCE
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PEPTIDE
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Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: (1) KININOGENS ARE INHIBITORS OF THIOL PROTEASES; (2)

-!- FUNCTION: (1) KININOGEN PREVALINED SOF THIOL PROTEASES; (2)

--- HWW-KININOGEN PLAYS AN IMPORTANT ROLE IN BLOOD COAGULATION BY

HELPING TO POSITION OPTIMALLY PRERALLIKEEIN AND FACTOR NEXT TO

FACTOR XII; (3) HWW-KININOGEN INHIBITS THE THROMBIN-AND PLASMIN-

INDUCED AGERGEATION OF THROMBON-YERS; (4) THE ACTIVE PEPTIDE

BRADKKININ THAT IS RELEASED FROM HWW-KININOGEN SHOWS A VARIETY OF

PHYSIOLOGICAL EFFECTS: (4A) INFLUENCE IN SMOOTH MUSCLE

CONTRACTION, (4B) INDUCTION OF HYPOTEBRION, (4C) NATRURESIS AND

DIURESIS, (4D) DECREASE IN BLOOD GLUCOSE LEVEL, (4E) IT IS A

MEDIATOR OF INFLAMMATION AND CAUSES (4E1) HURREASE IN VASCULAR

COTHER MEDIATORS OF INFLAMMATION (E.G. PROSTAGLANDINS), (4F) IT HAS

COTHER MEDIATORS OF INFLAMMATION OF COCCEPPORS (4E3) IT HAS

COTHER MEDIATORS OF INFLAMMATION OF REAXING FACTOR ACTION, (5)

LIMW-KININOGEN INHIBITS THE AGGREGATION OF THROMBOCYTES; (6) LMM-

KININOGEN IS IN CONTRAST TO HWW-KININOGEN NOT INVOLVED IN BLOOD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -:- SUBCELLULÀR LOCATION: Secreted.
-:- ALTERNATIVE PRODUCTS: 2 ISOFORMS; HWW (SHOWN HERE) AND LMW; ARE PRODUCED BY ALTERNATIVE SPLICING.
-:- TISSUE SPECIFICITY: PLASMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Takano M., Kondoh J., Yayama K., Okamoto H.;
"Molecular cloning of cDNAs for mouse low- and high- molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -> K (IN REF. 2).
D3172DF94FF56AF5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MISSING (IN ISOFORM LMW).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 38; DB 1;
Pred. No. 15;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KNG_MOUSE STANDARD; PRT; 661 AA. 008677; 008676; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Kininogen precursor [Contains: Bradykinin].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORMS HMW AND LAWW).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70933 MW;
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ilarity 75.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 IDTVKKATSQVV 312
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Best Local Similarity
9; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 IDNVKKARVQVV 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     639 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
28
83
107
1142
120
220
220
220
331
1127
1169
205
229
402
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomyces.
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259
322 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repeat; CBS domain.
                                           SEQUENCE FROM N.A.
                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                  SEQUENCE FROM N.A.
                        NCBI_TaxID=4932;
                                                                                                                                                                  protein kinase.
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                                                                                                                                                                                                       SMART; SM00043; CY; 3. PROSITE; PS00287; CY; 3. GASOTE; PS00287; CYSTATIN; 1. Glycoprotein; Plasma; Repeat; Thiol protease inhibitor; Vasodilator; Blood coagulation; Inflammatory response; Signal; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CEYKGRLSKAGAEPAPERQAESSQVKQ (IN ISOFORM
-!-*PTM: BRADYKININ IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN.
                                                                                                                                                                                                                                                                                                            CYSTATIN-LIKE 1.
CYSTATIN-LIKE 2.
CYSTATIN-LIKE 2.
CYSTATIN-LIKE 3.
HIS FACH.
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MISSING (IN ISOFORM LAW). 774460258D58796E CRC64;
                                                                                                                                                                                                                                                                        KININOGEN.
KININOGEN HEAVY CHAIN.
                                                                                                                                                                                                                                                                                                     KININOGEN LIGHT CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
16-0CT-2001 (Rel. 140, Last annotation update)
Nuclear protein SNF4 (Regulatory protein CAT3).
SNF4 OR CAT3 OR YGL115W.
Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                             BRADYKININ.
                                                                                                                                          InterPro; IPR000010; Cystatin.
InterPro; IPR003243; Cystatin_C_M.
InterPro; IPR002395; Kininogen.
                                                                                                                                                                         Pfam; PF00031; cystatin; 3.
PRINTS; PR00334; KININOGEN.
Probom; PD001231; Cystatin_C_M; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        661 NW; 73102 MW;
                                                                                                              EMBL; D84435; BAA19743.1; -. EMBL; D84415; BAA19742.1; -. MGD; MGI:1097705; Kng.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.9%;
ilarity 75.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300 IDTVKKATSQVV 311
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661 AA;
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Best Local Similarity
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P12904;
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DISULFID
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CARBOHYD
VARSPLIC
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               kinase.";
J. Biol. Chem. 269:2361-2364(1994).

J. Biol. Chem. 269:2361-2364(1994).

FUNCTION: THIS PROTEIN CAUSES EXPRESSION OF GLUCOSE-REPRESSIBLE GENES UPON GLUCOSE DEPRIVATION. IT INTERACTS AND HAS FUNCTIONAL RELATIONSHIP TO THE PROTEIN-KINASE SNFI.

-!- SUBCELLULAR LOCATION: Nuclear.

-!- SIMILARITY: BELONGS TO THE 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA SUBUNIT FAMILY.

-!- SIMILARITY: CONTAINS 4 CBS DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 30-34 AND 316-322.
MEDLINE=94131988; PubMed=7905477;
Mitchelhill K.I., Stapleton D., Gao G., House C., Michell B.,
Katsis F., Witters L.A., Kemp B.E.;
"Mammalian AMP-activated protein kinase shares structural and functional homology with the catalytic domain of yeast Snfl protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                       Schueller H.-J., Entian K.-D.; "Molecular characterization of yeast regulatory gene CAT3 necessary for glucose derepression and nuclear localization of its product."; Gene 67:247-257(1988).
                                                                                                                                                                                            MEDLINE-90097921; PubMed-2481228; Celenza J.L., Eng F.J., Carlison M.; Molecular analysis of the SNF4 gene of Saccharomyces cerevisiae: evidence for physical association of the SNF4 protein with the SNF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carbohydrate metabolism; Transcription regulation; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                             Lauguin G.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Doi A., Doi K.;
Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51B387E346EE9561 CRC64;
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Pred. No. 18;
3; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CBS 1.
CBS 2.
CBS 3.
CBS 4.
                                                                                                                                                                                                                                                                                                                                   Mol. Cell. Biol. 9:5045-5054(1989)
MEDLINE=89006284; PubMed=3049255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
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EMBL; M30470; AAA35061.1; --
EMBL; 272637; CAA96823.1; --
EMBL; D16506; BAA03958.1; --
PIR; JT0316; RGBYC3.
PIR; A33480; A33480.
SGD; S0003083; SNF4.
InterPro; IPR000644; CBS.
Pfam; PF00571; CBS; 4.
SMART; SM00116; CBS; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36401 MW;
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66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-21 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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175
246
318
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Best Local Similarity (
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Saccharomycetales; Saccharomycetaceae; Saccharomyces.
          NCBI_TaxID=4932;
                                                   STRAIN-YPH501;
                                                                                                                                                                                                                                                FORMATION.
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ID AX2E_PHAAU
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CONFLICT
CONFLICT
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                                                                                                                                                                                                                                                                      STRAIN=ATCC 8090;
Daggett Garvin L., Hardies S.C.;
Daggett Garvin L., Hardies S.C.;
Submitted (APR-1991) to the EMBL/GenBank/DDBJ databases.
Submitted (APR-1991) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE LEUCINE, ISOLEUCINE,
VALINE, (TRRENNINE) TRANSPORT SYSTEM, WHITCH IS ONE OF THE TWO
PERIPLASMIC BINDIN FOOTEIN-DEDENDENT TRANSPORT SYSTEMS OF THE
HIGH-AFFINITY TRANSPORT OF THE BRANCHED-CHAIN AMINO ACIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1995 (Rel. 31, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
T-complex protein 1, epsilon subunit (TCP-1-epsilon) (CCT-epsilon).
CCT5 OR TCP5 OR YJR064W OR J1752.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Periplasmic.
-!- SIMILARITY: BELONGS TO THE LEUCINE-BINDING PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62.5%; Score 35; DB 1; Length 367; 63.6%; Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino-acid transport; Transport; Periplasmic; Signal.
SIGNAL
1 23 BY SIMILARITY.
CHAIN
CHAIN
1 367 LEU/ILE/VAL-BINDING PROTEIN.
DISULFID 76 101 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F731F36CB64CAC19 CRC64;
                                                                                                                                        01-MAY-1992 (Rel. 22, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Leu/Ile/Val-binding protein precursor (LIV-BP)
                                                                                                    367 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        551 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; S14619; S14619.
HSSP; P02917; 2LIV.
InterPro; IPR001828; ANF_receptor.
Interpro; IPR000709; Leu_Ile_Val_bind.
Pfam; PF01094; ANF_receptor; 2.
PRINTS; PR00337; LEUILEVALBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                             01-MAY-1992 (Rel. 22, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     367 AA; 39087 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X58820; CAA41622.1; -. PIR; S14619; S14619.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 62.5
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                             Citrobacter freundli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 DNLKKANADVV 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 DNVKKARVQVV 12
                         :||::||||
284 MDNIRKARV 292
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
          1 IDNVKKARV 9
                                                                                                                                                                                                                                  NCBI_TaxID=546;
                                                                                                                                                                                                                     Citrobacter.
                                                                                                  LIVJ_CITFR
P25399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCPE_YEAST
ID TCPE_YEAST
AC P40413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                         RESULT 11
LIVJ_CITFR
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                                                                                                                                                                                                                                                                                  XI.";
Yeast 12:869-875(1996).
-!- FUNCTION: MOLECULAR CHAPERONE; ASSIST THE FOLDING OF PROTEINS UPON
ATP HYDROLYSIS. KNOWN TO PLAY A ROLE, IN VITRO, IN THE FOLDING OF
ACTIN AND TUBULIN. IN YEAST MAY PLAY A ROLE IN MITOTIC SPINDLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: HETERO-OLIGOMERIC COMPLEX OF ABOUT 850 TO 900 kDa THAT
                                                                                                                                                                            MEDLINE-96437976; PubMed-8840504; Mandy M.E., Manus V., Chuat J.-C., Galibert F.; "Analysis of a 62 kb MA sequence of chromosome X reveals 36 open reading frames and a gene cluster with a counterpart on chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     024543;
16-027-2001 (Rel. 40, Created)
16-027-2001 (Rel. 40, Last sequence update)
16-027-2001 (Rel. 40, Last annotation update)
Auxin-induced protein 22E (Indole-3-acetic acid induced protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chaperone; ATP-binding; Multigene family.

CONFLICT 16 16 R -> T (IN REF. 1).

CONFLICT 47 47 A -> D (IN REF. 1).

CONFLICT 81 81 S -> T (IN REF. 1).

CONFLICT 263 268 CPFEPP -> VHLNLL (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                   Kim S.;
Submitted (XXX-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FORMS TWO STACKED RINGS, 12 TO 16 NM IN DIAMETER.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE TCP-1 CHAPERONIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B3B39B41ED05BF42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L -> I (IN REF. 1)
G -> N (IN REF. 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 35; DB 1;
Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  203 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60676 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   299 IDDVKKAGADVV 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 IDNVKKARVQVV 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                              SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
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193 VDNTLRARLEIV 204
                                                                                                                                                                                                                                                                                             1 IDNVKKARVQVV 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-1148;
                                                                                                                                                                                                                                                                                                                                                                                              GRPE_SYNY3
Q59978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
GRPE_SYNY3
          ò
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                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation-the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murphy L., Harris D., Barrell B.G., Rajandream M.A., Walsh S.V.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases
-!- FUNCTION: SUBUNIT OF THE PERIPHERAL VI COMPLEX OF VACUOLAR ATPASE
ESSENTIAL FOR ASSEMBLY OR CATALYTIC FUNCTION: V-ATPASE IS
RESPONSIBLE FOR ALIDIFYING A VARIETY OF INTRACELLULAR COMPARTMENTS
IN EUKARYOTIC CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peripheral catalytic V1 complex (components A to H) attached to an integral membrane V0 proton pore complex (components: a, c, c', c', and d) (By similarity).

SIMILARITY: BELONGS TO THE V-ATPASE E SUBUNIT FAMILY.
AUXŽE OR ARG14.
Phaseolus aureus (Mung bean) (Vigna radiata).
Phaseolus aureus (Mung bean) (Vigna radiata).
Bukaryota; Viridiplantas; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Spermatophyta; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                    Hashimoto H., Yamamoto K.T.;
"Intree more members of the Aux/IAA gene family from mung bean (Vigna
                                                                                                                                                                                        MEDIATION: COULD ACT AS REGULATOR OF GENES RESPONSIBLE FOR MEDIATING THE VARIOUS AUXIN-INDUCED EVENTS RESPONSIBLE FOR CELL GENOWITH (BY SIMILIARITY).

-1 SUBCELLULAR LOCATION: Nuclear (By similarity).

-1 INDUCTION: BY AUXIN.

-1 SIMILARITY: BELONGS TO THE AUX/IAA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (V-ATPase E subunit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: V-ATPase is an heteromultimeric enzyme composed of a peripheral catalytic V1 complex (components A to H) attached t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-CT-2001 (Rel. 40, Last annotation update)
48-COT-2001 (Rel. 40, Last annotation update)
(Vacuolar ATP Synthase subunit E (EC 3.6.3.14) (V-ATPase E St Vacuolar proton pump E subunit) (V-ATPase 26 kDa subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60.7%; Score 34; DB 1; Length 203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22694 MW; 4B13504E5A191F49 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        227 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                               (In) Plant Gene Register PGR97-137
                                                                                                                                                                                                                                                                                                                                                                                                                         Mendel; 25713; Phaau;1524;25713.
InterPro; IPR003311; AUX_IAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3;
                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AB004933; BAA20849.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 63.0%
Tr. Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF02309; AUX_IAA;
SEQUENCE 203 AA; 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 DNVKKARVQVV 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1:1: 1:1111
72 DSVQPAKVQVV 82
                                                                                                                                                                radiata) hypocotyl
                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                      TISSUE-Hypocotyl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VATE_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      013687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb region from map positions 64% to 92% of the genome.";
DNA Res. 2:153-166(1995).
-!- FUNCTION: STIMULATES, JOINTLY WITH DNAJ, THE ATPASE ACTIVITY OF DNAK. HELPS TO RELEASE ADP FROM DNAK THUS ALLOWING DNAK TO RECYCLE MORE EFFICIENTLY (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE GRPE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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MEDLINE-96127529; Pubmed-8590279;
MEDLINE-96127529; A. Sato S., Kotani H., Sazuka T., Miyajima N.,
Sugiura M., Tabata S.;
"Sequence analysis of the genome of the unicellular cyanobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 34; DB 1; Length 227;
Pred. No. 30;
5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.7%; Score 34; DB 1; Length 249; 45.5%; Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                            synthesis; Hydrogen ion transport,
AA; 25741 MW; B5180B4FC02080CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chaperone, Heat shock; Complete proteome.
SEQUENCE 249 AA; 27567 MW; C69CB5D0EB39B248 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OGT-2001 (Rel. 40, Last annotation update)
GRPE protein (HSP-70 cofactor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                        InterPro; IPPG0442; VATP-synt_E.
Pfam; PF01991; VATP-synt_E: 1.
Hydrolase; ATP synthesis; Hydroger
SEQUENCE 227 AA; 25741 MW ner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00773; GRPEPROTEIN. PROSITE; PS01071; GRPE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.78;
                                                                                                                                                                                                                                                                                 EMBL; Z98595; CAB11186.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D64001; BAA10291.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000740; GrpE. Pfam; PF01025; GrpE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 60.7
Best Local Similarity 41.7
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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1 IDNVKKARVQV 11 :|| ::|| |: 137 VDNFERARTQI 147

Oy Op

Search completed: July 1, 2002, 16:30:13 Job time: 622 sec

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OGFDR2
388
62.5
3
                                                                                                                 July 1, 2002, 16:29:45; Search time 75.26 Seconds (without alignments) 27.584 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                            562222
                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                   562222 seqs, 172994929 residues
                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_vertebrate:*
sp_unclassified:*
sp_vvirus:*
sp_bacteriap:*
sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp_mhc:*
sp_organelle:*
sp_phage:*
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56
1 IDNVKKARVQVV 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sp_plant:*
sp_rodent:*
sp_virus:*
                                                                                                                                                                                          Title:
Perfect score;
Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database :
                                                                                                                                                                                                                                                                                                                    Searched:
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SUMMARIES

Description	O96220 plasmodium	058817 pyrococcus	032330 clostridium	P70517 rattus norv	063581 rattus norv	091xk5 mus musculu	091ms5 lumpy skin	0971v5 sulfolobus	O26858 trvpanosoma	046508 desulforibr	09ff22 arabidopsis	092d88 listeria in	09x250 thermotoga	093kz5 burkholderi	091q13 orvza sativ	0930wl rhizobium m
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Score	40	39	38	38	38	38	37	36	36	36	35	35	35	35	35	32
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Query Match
71.4%; Score 40; DB 5; Length 540;
Best Local Similarity 66.7%; Pred. No. 33;
Matches 8; Conservative 1; Mismatches 3; Indels

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00017770170000000000000000000000000000	0907P0 0907P0 09X299 ALIGN	PRT;	Created) Last sectost ann FOLD SUPE	4551; arucci E	G. B.
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666 66 66 66 66 66 66 66 66 66 66 66 66	, o, o,	RELI	99 (TrEM) 99 (TrEM) 11 (TrEM) PROTEIN	N.A N.A 743; Tet Joy	zhou seque seque 126-1 7, AA 30242 ; cpn 54; T
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PEQUENCE FROM N.A.

***X EXCUENCE FROM N.A.

***X MEDLINE-85127561; PubMed-2578992;

***X Cole T., Inglis A.S., Roxburgh C.M., Howlett G.J., Schreiber G.;

***A Cole T., Inglis A.S., Roxburgh C.M., Howlett G.J., Schreiber G.;

***A "Major acute phase alphal-protein of the rat is homologous to bovine

***X Major acute phase alphal-protein of the rat is homologous to bovine

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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
MAJOR ACUTE PHASE ALPHA-1 PROTEIN PRECURSOR (FRAGMENT).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
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Rattus norvegicus (Rat).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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MEDLINE-85149311; PubMed=2579644;
Cole T., Inglis A., Nagashima M., Schreiber G.;
"Major acute-phase alpha(1)-protein in the rat: Structure, molecular cloning, and regulation of mRNA levels.",
Biochem. Biophys. Res. Commun. 126:719-724(1985).
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01-NOV-1996 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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SEQUENCE FROM N.A.
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A Rawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,

A Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,

A Ramanoto S., Sekhine M., Baba S.-I., Kosuqi H., Hosoyama A., Nagai Y.,

Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,

Punahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,

Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,

Masuchi Y., Shizuya H., Kikuchi H.;

"Complete sequence and gene organization of the genome of a hyper-
thermophilic archaebacterium, Pyrococcus horikoshii OT3.";

DNA Res. 5:55-76(1998).

"R EMBL, AP000004; BAA30189:1, -.

R InterPro: IPR005629; Methionine Synt.

R Fam; PF01717; Methionine—Synt:

R Pfam; PF01717; Methionine—Synt:

W Hypothetical protein; Complete proteome.

SEQUENCE 309 AA; 35509 WW; 88ABAA43D2C7522D CRC64;
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NCBI_TaxID=53953;
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MEDLINE-98053837; PubMed-9393688;
Heath R.J., Goldfine H., Rock C.O.;
"A gene (plsD) from Clostridium butyricum that functionally substitutes for the sn-glycerol-3-phosphate acyltransferase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clostridium butyricum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
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                                                                                                               01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 35.5 KDA PROTEIN PH1090.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE.
                                                             309 AA.
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Pred. No. 28;
5; Mismatches
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J. Bacteriol. 179:7257-7263 (1997).
EMBL; AF009362; AA446006.1;
InterPro; IPR002123; Acyltransferase.
Pfam; PF01553; Acyltransferase; 1.
Transferase; Acyltransferase; 1.
SEQUENCE 234 AA; 2619
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54.5%;
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Best Local Similarity 54.5
Matches 6; Conservative
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ENLKKARIKVI 56
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"High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
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STRAIN=NEETHLING 2490;
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-C57BL/6J, TISSUE-PLACENTA;

Arakawa T., Alzawa K., Akahira S., Akimura T., Aono H., Arai A.,

A Arakawa T., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,

Imotani K., Ishii Y., Itoh M., Izawa M., Kato H., Kawai J., Kojima Y.,

Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A.,

Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A.,

Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T.,

Owa C., Saito H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D.,

An Shibata K., Shibata Y., Shinaqawa A., Shiraki T., Soqabe Y.,

Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y.,

Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,

Muramatsu M., Hayashizaki Y.;

Submitted (JUL-2000) to the EMBL/GenBank/DDbJ databases.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last senotation update)
ADULT FEMALE PLACENTA CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
CLONE:1600027101, FULL INSER SEQUENCE.
ENAS musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIKEN FANTOM Consortium.; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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                        MEDLINE-01004 1.7.

Anderson K.P., Croyle M.L., Lingrel J.B.;
Anderson K.P., Croyle M.L., Lingrel J.B.;
Primary Structure of a gene encoding rat T-kininogen.";
Gene Bill: 119-128 (1989).
REMBL; M29090; AAA42251.1; -..
REMBL; M29091; AAA42251.1; JOINED.
REMBL; M29091; AAA42251.1; JOINED.
REMBL; M29085; AAA42251.1; JOINED.
REMBL; M29085; AAA42251.1; JOINED.
REMBL; M29088; AAA42251.1; JOINED.
REMBL; M29089; AAA42251.1; JOINED.
REMBL; M29089; AAA42251.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                            11; Length 430;
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                                                                                                                                                                                                                                                                                                                                                                         Score 38; DB 1
Pred. No. 62;
0; Mismatches
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MEDLINE-21085660; PubMed=11217851;
                                                                                                                                                                                                                                                         Pfam; PF00031; cystatin; 3.
Probom; PD001231; cystatin_C_M; 1.
SMART; SM00043; CY; 3.
PR0STTE; PS00287; CYSTAIIN; 2.
SEQUENCE 430 AA; 47618 WW; 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-CS7BL/GJ; TISSUE-PLACENTA;
PEDLINE-99279253; Pubmed-10349636;
Carningi P., Rayashizaki Y.;
                                                                                                                                                                                                                                 InterPro; IPR000010; Cystatin.
InterPro; IPR003243; Cystatin_C_M.
                                                                                                                                                                                                                                                                                                                                                                         67.9%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                          9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                    1 IDNVKKARVQVV 12
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Best Local Similarity
Matches 9; Conserv
[1]
SEQUENCE FROM N.A.
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SEQUENCE FROM N.A..

SEQUENCE FROM N.A..

SEQUENCE TISSUE-PLACENTA;

MEDLINE-20530913; PubMed-11076861;

Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,

Ronno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

Ronno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

Ronno H., Akiyama J., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto H., Sakaguchi S., Ikeqami T., Kashiwagi K.,

Rujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

Rujiwake S., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

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RIKEN integrated Sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";

Genome Res. 10:1757-171(2000).

REMBL; AKO0547; BAB24115.1;

SEQUENCE 432 AA; 47898 WW; 91854EDA5284A16B CRC64;
SEQUENCE FROM N.A.
STRAIN-C57BL/61; TISSUB-PLACENTA;
MEDLINE-20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
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Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF325528; AAK85048.1; -.
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MEDLINE-21329495; PubMed=11435593;
Tulman E.R., Afonso C.L., Lu Z., Zsak L., Kutish G.F., Rock "Genome of lumpy skin disease virus.";
J. Virol. 75:7122-7130(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.1%; Score 37; DB 12; Length 253; 50.0%; Pred. No. 55; ive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
LSDV087 MOTT MOTIF PUTATIVE GENE EXPRESSION REGULATOR.
LSDV087.
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253 AA; 30004 MW; 22D2573CA0BEA3B2 CRC64;
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63;
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Pred. No. 63;
0; Mismatches
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Best Local Similarity 75.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lumpy skin disease virus.
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Gaps

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RESULT

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O9FF22;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
6ENOMIC DNA, CHROMSOME 5, Pl CLONE:MXII0.
Arabidopsis thaliana (Mouse-ear cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Characterization of an operon encoding an NADP-reducing hydrogenase
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BEDLINE-27471969; PubMed-9330910;
Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,
Miyajima N., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-95270577; PubMed-7751270;
MENLY S., Saimmaime I., De Luca G., Rousset M., Dermoun Z.,
Belaich J.P.;
                                                                                                                                                                                                                                                                                                                                            Desulfovibrio fructosovorans.
Bacteria; Proteobacteria; delta subdivision; Desulfovibrio.
                       Length 544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
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eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
POTENTIAL NAD-REDUCING HYDROGENASE SUBUNIT.
                     Score 36; DB 5; Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 36; DB 2;
Pred. No. 2e+02;
                                                                                                                                                                                                                                 585 AA.
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                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00198; 4FE4S_FERREDOXIN; 1.
Iron-sulfur.
SEQUENCE 585 AA; 63429 MW; C14D0EF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001450; 4Fe4S_ferredoxin.
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                                                                                                                                                                                                                                 PRT;
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IPR003149; Fe_hyd_SSU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in Desulfovibrio fructosovorans."
J. Bacteriol. 177:2628-2636(1995)
EMBL: U07229; AAA87057.1; -.
HSSP; P29166; IFEH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR001041; Ferredoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3;
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Pfam; PF02256; Fe_hyd_SSU; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64.3%;
63.6%;
                     64.3%;
58.3%;
                                                           Conservative
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                                                                                                                                                                                                                                 PRELIMINARY;
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Pfam; PF00037; fer4; 1
                                                                                               1 IDNVKKARVQVV 12
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25 LENLKVAQVQVV 36
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Best Local Similarity
7; Conserve
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                                       Best Local Similarity Matches 7; Conserv
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NCBL_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=878;
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InterPro;
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                       Query Match
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Q46508;
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
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"Characterization of glucose transport and cloning of a hexose
transporter gene in Trypanosoma cruzl.",
Proc. Natl. Acad. Sci. U.S.A. 918278-8282(1994).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
                                                                                                                                                                                                          ST1243.
Sulfolous tokodail.
Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.
NGBI_TaxID=111955;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17; Length 220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence of an aerobic thermoacidophilic Crenarchaeon, Sulfolobus tokodail strain?.";
DNA Res. 8:123-140(2001).
EMBL; AP000985; BAB66284.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 220 AA; 24964 MW; 1776CA9DE0D54347 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
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                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL PROTEIN ST1243.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                             220 AA.
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Pred. No. 72;
5; Mismatches
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InterPro, IPR003663; Sugar_transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00171; SUGRTRNSPORT.
PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
                                                                                                                                  Created)
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                                                                                             PRT;
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PRINTS; PR00171; SUGRTRNSPORT
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41.78;
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
HEXOSE TRANSPORTER.
                                                                                                                                01-DEC-2001 (TrEMBLrel. 19,
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                                                                                             PRELIMINARY;
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STRAIN=JCM 10545 / 7;
PubMed=11572479;
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175 LDNIRKNRIEAV 186
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43 LDNVKKVSISIV
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    NCBI_TaxID=2336;
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DubMed=11679669.

A Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,

A Glaser P., Bloecker H., Brandt P., Chakraborty T.,

Charbit A., Chetouani F., Couve B., de Daruvar A., Dehoux P.,

Domann E., Dominguez Bernal G., Duchaud E., Durant L., Dussurget O.,

Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,

A Bautler L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurspkat G.,

Madueno E., Maitournam A., Mata Vicente J., Ny B., Nedjari H.,

Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

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Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;

Comparative genomics of Listeria species.";

EMBL; AL596166; CAC96161.; -.
"Structural analysis of Arabidopsis thallana chromosome 5. I. Sequence features of the 1.6 Mb regions covered by twenty physically assigned
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Pred. No. 1.1e+02;
3; Mismatches 3; Indels
                                                                                                                     2; Indels
                                  DNA Res. 4:215-230(1997).
EMBL; AB005248; BAB09352.1; -.
SEQUENCE 151 AA; 18044 MW; C2C20F06F3385B3B CRC64;
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01-NAY-2000 (TrEMBLrel. 13, Last annotation update)
HYPOTHETICAL 29.9 KDA PROTEIN.
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Pred. No. 75;
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STRAIN-WISB / DSM 3109;
MEDINIE-99287316; PubMed-10360571;
MEDSON K.E., Clayton R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
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"Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
Mature 399:323-329(1999).
TIGR: TM1727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Winstanley C., Hales B.A., Hart C.A.;
"Evidence for the presence in Burkholderia pseudomallel of a type III
"Evidence for the presence in Burkholderia secretion system-associated gene cluster.";
J. Med. Microbiol. 48:649-656(1999).
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"Distribution of type III secretion gene clusters in Burkholderia pseudomallei, Burkholderia thailandensis and Burkholderia mallei."; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF074878; AAK73326.1; -. SEQUENCE 274 AA; 29653 MW; 727AE95D20EA5FA4 CRC64;
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Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
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Pred. No. 1.4e+02;
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66.7%; Pred. No. 1.4e+02;
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264 AA; 29883 MW; 3ABD9A420A4E7FE7 CRC64;
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S. epidermidis ope Plasmodium falcipa Anti-angiogenic D3

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Composition for inhibiting angiogenesis and endothelial cell proliferation, inducing endothelial cell apoptosis and treating cancer,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anti-angiogenic peptide C-terminal fragment
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AAP40633
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AAG82639
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AAG81510
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AAU34090
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries

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AAR33350
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ABG21101
ABG21099
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                      A_Geneseq_032802:*
                                                                                                                                                                     1 IDNVKKARVQVV 12
                                                                                                                                 US-09-461-061A-3
                                                                                                                                                                                                                                                                                         seq length: 0
seq length: 2000000000
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rheumatoid arthritis, and ocular disorders comprises a kininogen domain
                                               The present sequence is that of a C-terminal fragment of a novel anti-anglogenic D3 peptide (see AAY95408) derived from human high mol.wt. kininogen (HK) domain 3 (see AAY95426). The full-length D3 peptide inhibits endothelial cell proliferation and thus possesses anti-anglogenic activity. It is an example of peptides of the invention (see AAY95405-26) that are analogues of certain sites in the HK domain 3. The peptides inhibit endothelial cell proliferation and may also induce endothelial cell apoptosis. Compositions including the peptides are used in claimed methods for inhibiting anglogenesis, inhibiting endothelial cell proliferation, and inducing endothelial cell apoptosis. Cancer, rheumatoid arthritis, and ocular disorders characterized by undesired vascularization of the retina are treated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The specification describes a method for identifying a peptide having
                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        function, useful particularly for database for combination of nucle
                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                               Precursor peptide; polypeptide hormone; peptide identification
                                                                                                                                                                                                                                        Length 12;
                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide identified from an origin of prepro-bradykinine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Berge G,
                                                                                                                                                                                                                                      Score 56; DB 21;
Pred. No. 0.00033;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Martinez J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SCRC ) SCRAS SOC CONSEILS RECH & APPL SCI (CNRS ) CNRS CENT NAT RECH SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "hydrogen attached"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "amidated residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying peptide with selected C-amidated hormones, by screening
                                                                                                                                                                                                                                                                                                                                                          AAB08553 standard; Peptide; 16 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Camara Ferrer YJA, Thurieau C,
                               Claim 3; Page 25; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 16; Page 20; 40pp; French.
                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acid and amino acid sequences
                                                                                                                                                                                                                                    100.0%;
llarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-FEB-2000; 2000WO-FR00460.
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                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                             1 IDNVKKARVQVV 12
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                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                     20-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-AUG-2000
                                                                                                                                                                                                         Seguence
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            analog
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thrombin-induced platelet; prevention; platelet aggregation;
a particular function. The method comprises preparing a database of polynucleotides and polypeptides of unknown functions, screening the database for a combination of nucleotides or amino acids indicative of the peptide with a particular function, and identifying polynucleotides and proteins which contain the peptide. The method is used to identify precursor peptides with an amidated C-terminus, especially polypeptide hormones, for studying physiologically active substances. The present sequence represents a peptide which was identified using the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Administration of a peptide or multimer related to bradykinin or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disclosed peptides and multimers can be used for the inhibition of thrombin-induced platelets or other cells. They can also be used for preventing platelet aggregation, or inhibiting ADP-induced activation. This is useful to prevent arterial occlusions arising from coronary thrombosis and stroke.
                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    new
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inhibition of platelet activation and aggregation - by admin. of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                            Length 16;
                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                               100.0%; Score 56; DB 21;
ilarity 100.0%; Pred. No. 0.00045;
Conservative 0; Mismatches 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 44; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW54336 standard; peptide; 26 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bradykinin analogous peptide 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or known bradykinin analogues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95us-00000096.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schmaier AH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inhibition; thrombin-ir
ADP-induced activation
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                                                                                                                                                                                                                                                                                                                                                                                                                          1 IDNVKKARVQVV 12
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Best Local Similarity
Thes 12; Conserve
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                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                    16 AA;
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                                                                                                                                                                                                      the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 - DEC - 1996
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                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW54336
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AAY95408 RESULT

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the human kininogen heavy chain. Domain 3 was isolated from low molecular weighth kininogen, derived from human plasma, by cleavage with trypsin. Domain 3 peptide inhibits platelet activation causing a marked decrease in the platelets ability to aggregate and secrete their granule contents. The granule contents contents properlies proteins which participate in hemostasis, thrombosis and the inflammatory response. Domain 3 also inhibits endothelial cell activation shown by a decrease
                                                         Domain 3; human; kininogen; heavy chain; low molecular weight; plasma; trypsin; platelet; activation; granule contents; hemostasis; thrombin; tissue plasminogen activator;thrombosis; inflammatory response; endothelial cell; von Willebrand factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in secretion of endothelial cell contents such as tissue plasminogen activator and von Milebrand factor. Domain 3 functions to inhibit cell activation by blocking thrombin binding to its target cells, the peptide is a selective inhibitor of thrombin-induced plattlet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence given represents domain 3, amino acids 246-362, of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 56; DB 14; Length 117; 100.0%; Pred. No. 0.004; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of trypsin-cleavage fragment of human kininogen - for increasing vascular bradykinin release, for lowering blood pressure and treating hypertension
                   Domaine 3, bradykinin release activating peptide.
                                                                                                                                                                                                                                    1..18
/note= "Leader peptide"
                                                                                                                                                                                                                                                                                              /note= "Mature protein"
                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB37447 standard; protein; 122 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 1; 46pp; English.
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                                                                                                                                                                                                                                                                        19..117
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38 idnvkkarvqvv 49
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Matches 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 AA;
                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                          13-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-FEB-2001
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                                                                                                                                                                                                                                  Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Composition for inhibiting angiogenesis and endothelial cell proliferation, inducing endothelial cell apoptosis and treating cancer, rheumatoid arthritis, and ocular disorders comprises a kininogen domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is that of a D3 peptide derived from human high mol.wt. kiningen (HK) domain 3 (see AAY95426). The D3 peptide inhibits endothelial cell proliferation and thus possesses anti-angiogenic activity. It is an example of D3 peptides of the invention (see AAY95405-26) that are analogues of certain sites in the H domain 3, in this case amino acid residues Asn275-Lys282. The peptides inhibit endothelial cell proliferation and may also induce endothelial cell apoptosis. Compositions including the peptides are used in claimed methods for inhibiting angiogenesis, inhibiting endothelial cell proliferation, and inducing endothelial cell apoptosis. Cancer, rheumatchid arthritis, and ocular disorders cell apoptosis. Cancer, rheumatchid arthritis, and ocular disorders cell apoptosis.
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                                                                                                                                                                                                                                                 Anti-angiogenic; angiogenesis; inhibitor; kininogen; homologue; andothelial cell proliferation; apoptosis; cancer; ocular disorder; rheumatoid arthritis; cytostatic; antiarthritic; antirheumatic; therapy; human; 03 peptide.
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                                                                           AAY95408 standard; Peptide; 32 AA
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                                                                                                                                                                                                         Anti-anglogenic D3 peptide
                                                                                                                                                                 (first entry)
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Best Local Similarity 100.
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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Composition for inhibiting angiogenesis and endothelial cell proliferation, inducing endothelial cell apoptosis and treating cancer, rheumatoid arthritis, and ocular disorders comprises a kininogen domain
                                                                                                                                                                        The present sequence is that of domain 3 of human high mol.wt. kininogen (HK). The invention provides peptides (see AAV95405-24) that are analogues of certain sites in the HK domain 3, specifically Asn275-Lys282, Cys246-Cys249, Leu331-Tyr338 and Tyr299-Ser314. The peptides, in which native Cys residues may be replaced by Ala residues, inhibit endothelial cell proliferation and may also induce endothelial cell apoptosis. Compositions including the peptides are used in claimed methods for inhibiting angiogenesis, inhibiting endothelial cell apoptosis. and inducing endothelial cell apoptosis. Cancer, rheumatoid arthritis, and coular disorders characterized by undesired vascularization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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100.0%; Pred. No. 0.0042;
ive 0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human diagnostic protein #21092
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                                                                                                                                           Disclosure; Page 4; 44pp; English.
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23-AUG-2000; 2000US-0649167
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Best Local Similarity 100.

Matches 12; Conservative
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N-PSDB; AAS85288.
WPI; 2000-442247/38.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              123 AA;
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                                                                                                                                                                                                                                                                                                                                          Inhibition of mammalian legumain or legumain-related endopeptidase by cystatin involves interaction with second papain-non-reactive site of
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                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 4; 45pp; English.
                                                                                                                                       20-APR-2000; 2000WO-GB01571.
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Matches 12; Conservative
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                    Homo sapiens.
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Query Match

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polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymcleotides are also used in diagnostics as expressed sequence tags: polymcleotides are also used in diagnostics as expressed sequence tags to reactor normal activity of (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving cuantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymcleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations ceptor produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequence of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO. at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome
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Pred. No. 0.081;
0; Mismatches 0; Indels
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Best Local Similarity 100.0
Matches 11; Conservative
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polypeptide (II) sequences. (I) is useful as hybridisation probes, and gone mapping, and in recombinant production of (II). The and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques of restranger for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and among a milno acid sequences of the invention.

Conduction in the printed diagnostic anno acid sequences of the invention.

Conduction in the printed conducts dependent on but and diagnostic anno acid sequences of the invention.
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23-AUG-2000; 2000US-0649167.
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Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                             644 AA;
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         polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (1) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). Is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                       and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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Pred. No. 0.097;
1; Mismatches 0; Indels
and gene mapping, and in recombinant production of (II).
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                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG21102 standard; Protein; 248 AA.
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91.78;
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23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                 Local Similarity 91.7
                                                                                                                                                                                                                                                                                                                                                                 305 idnvkkarvrvv 316
                                                                                                                                                                                                                                                                                                                                          1 IDNVKKARVQVV 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-639362/73.
N-PSDB; AAS85289.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drmanac RT, Liu C,
                                                                                                                                                                                                                                                 435 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-0CT-2001.
                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG21102;
                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                        ABG21102
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polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (1) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as
                                                                                                                                                                                  a food supplement. (1) and its binding partners are useful in medical imaging of sites expressing (II). (1) and (II) are useful in medical imaging of sites expressing (II). (1) and (II) are useful for treating discretes involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bradykinin is a peptide consisting of nine amino acids. It has the biological effect of decreasing blood pressure. Although kininogen is known as a protein-precursor of bradykinin, its structure is unknown because of the difficulty in collecting large enough samples of kininogen for structural investigation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85.7%; Score 48; DB 22; Length 248; 100.0%; Pred. No. 0.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          378..386
/label- bradykinin
391..395
/note= "probe (AAN40241)-encoded sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bradykinin protein precursor: type II (pKG146, pKG254).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 0.3
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAP40633 standard; Protein; 434 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Blood pressure; kininogen; probe..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 2; 6 pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MITU ) MITSUBISHI CHEM IND KK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1984-216122/35.
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Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IDNVKKARVQ 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           248 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              434 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAN40314
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Till, given in AAG81454 to AAG81320, from Staphylococcus epidermidis.

(I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the S. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their certainty and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH55971 to AAH55090 represent oligonucleotide sequences from the present invention. AAH55091 to AAH56098 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present for SEQ ID NO:4455 to 4464.
                                                                                                                                                                                                                                                                                                                                                                                AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine; antimalarial; malaria; protozoacide; infection; insecticide.
                                                                                                                                                                                                                                                                                                     Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium falciparum chromosome 2 related protein SEQ ID NO:126
epidermidis SR1 strain; infection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 40; DB 2
Pred. No. 6.1;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                  Claim 18; Page 627; 2188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB18269 standard; Protein; 540 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71.4%;
75.0%;
                                                                                                                                   09-NOV-2000; 2000WO-US30782.
                                                                                                                                                                  99US-0164258
                                            Staphylococcus epidermidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
Staphylococcus epidermidis vaccination; endocarditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                (GLAX ) GLAXO GROUP LTD.
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124 idnvkkttvyvv 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 IDNVKKARVQVV 12
                                                                                                                                                                                                                                                         WPI; 2001-316495/33.
N-PSDB; AAH53489.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 9; Conserv
                                                                         WO200134809-A2
                                                                                                                                                                  09-NOV-1999;
                                                                                                                                                                                                                              Kimmerly WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bradykinin is a peptide consisting of nine amino acids. It has the biological effect of decreasing blood pressure. Although kininogen is known as a protein-precursor of bradykinin, its structure is unknown because of the difficulty in collecting large enough samples of kininogen for structural investigation.
                                            Gaps
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    epidermidis open reading frame protein sequence SEQ ID NO:2372.

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              Length 434;
                                            Indels
                                                                                                                                                                                                                                                                       Bradykinin protein precursor: type I (pKG13, pKG59).
           Score 44; DB 5;
Pred. No. 3.2;
); Mismatches
                                                                                                                                                                                                                                                                                                                                  380..388
/label= bradykinin
/333..397
                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                             AAP40257 standard; Protein; 436 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 2; 6 pp; Japanese.
                                                                                                                                                                                                                                                                                                    Blood pressure; kininogen; probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MITU ) MITSUBISHI CHEM IND KK
            78.6%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83JP-0000984
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           Query Match 78.6
Best Local Similarity 83.3
Matches 10; Conservative
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                                                                                        || |||| ||||
298 idtvkkatvqvv 309
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                436 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAN40242
                                                                                                                                                                                                                                                                                                                                                                                                                           JP59125896-A
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                                                                                                                                                                                                           AAP40257;
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                                                                                                                                                                                                                                                                                                                                                Peptide
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                                                                                                                                                RESULT 13
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                                                                                                                                                              AAP40257
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The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum. Also described are: (I) nucleotide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comppising (I) or (II).

(I) and (II) are useful for the development of vaccines against P. falciparum infection. (I) and polycional antisera or a monoclonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of farget treat or prevent P. falciparum infection, or they can be used to identify drug resistance in confection, or they can be used to identify drug resistance in complexity of the parasite biology, a process hampered by the subsequent identification of proteins encoded by it will help to expand complexity of the parasite biology, a process hampered by the complexity of the parasite lifecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and mosquito and protein sequences given in the pressing incention, but which are not
                                                                                                                                                                                                                                                                                                                                                              Proteins encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum, useful as antimalarial vaccines and in the diagnosis of P.falciparum infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71.4%; Score 40; DB 21; Length 540; 66.7%; Pred. No. 23; 3; Indels iive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               specifically mentioned within the specification
                                                                                                                                                                                                                                                                                 Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 296-298; 577pp; English.
                                                                                                                                                                                                                                                                             Gardner M,
                                                                                   99WO-US26796
                                                                                                                           98US-0107131
                                                                                                                                                                                                                                                                           Hoffman S, Carucci D,
                                                                                                                                                                   (HOFF/) HOFFMAN S.
(CARU/) CARUCCI D.
(GARD/) GARDNER M.
(VENT/) VENTER J C.
                                                                                                                                                                                                                                                                                                                       WPI; 2000-365347/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       540 AA;
WO200025728-A2
                                                                                   05-NOV-1999;
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                                        11-MAY-2000.
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Query Match
Best Local Similarity 66.77
Matches 8; Conservative ||| ||| |: 277 idnfkkanvdvi 288 1 IDNVKKARVQVV 12 δ

; 0

Gaps

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Search completed: July 1, 2002, 16:19:44 Job time: 148 sec

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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 1, 2002, 16:17:16 ; Search time 46.58 Seconds
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Run on: July 1, 2002, 16:17:16; Search time 46.58 Seconds

(without alignments)
16.503 Million cell updates/sec
Title: US-09-461-061A-1
Perfect score: 45
Sequence: 1 NNATFYFK 8
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

283138 seqs, 96089334 residues

Searched:

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database: PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	kiningan, TMM pre	HWM	en, le	I MMI		telomerase reverse	hypothetical prote		Ω	hypothetical prote	⊆	NADH denydrogenase	probable cytochrom	hypothetical prote	hypothetical prote	υ	hypothetical prote			G)	hypothetical prote	hypothetical prote	⊆	secretory protein	invasion protein i		III	dehy	hypothetical prote
SUMMARIES		KGHUL1	КСНОН1	A28055	A25486	T24062	T31107	T24206	B83803	T06978	F86924	A86650	T11319	G96611	T25830	T31994	Н97322	T32658	T01483	F69403	S70849	D84466	T23191	A40774	AF0852	S54420	E91095	A85941	T10982	T25078
	DB	: :	-	7	~	~	~	~	7	~	~	~	7	~	~	~	~	7	~	7	7	~	7	~	7	7	a	7	N	7
	Length	427	644	433	639	828	1132	182	71	182	273	319	440	497	630	758	949	303	332	469	603	206	892	484	562	563	267	267	909	1215
đ	Query Match	100.0	100.0	86.7	86.7	80.0	80.0	77.8	75.6	75.6	75.6	75.6	75.6	75.6	75.6	75.6	75.6	73.3	73.3	73.3	73.3	73.3	73.3	71.1	71.1	71.1	71.1	71.1	71.1	71.1
	Score	45			39			32	34	34	34	34	34	34	34	34	34	33	33	33	33	33			32				32	
	Result No.	п	7	m	4	S.	ڣ	7	œ	თ	10	11	12	13	14	12	16	17	18	19	20	21	22	23	24	25	56	27	28	29

protein kinase GCN cytokinin-induced	hypothetical prote hypothetical prote	hypothetical prote amidotransferase h	probable permease hypothetical prote	U2 snRNP auxiliary	conserved hypothet conserved hypothet	U2 small nuclear r	N-acetyl-gamma-glu	N-acetyl-gamma-glu	N-acetyl-gamma-glu	outer membrane pro
OKBYN2 T10059	B71529 E90088	F84366 F84941	AF0604 T34501	A46179	F69409 S59078	JC6125	RDECEP	G91239	D86087	A82299
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1659	148 171	190 196	202	240	249 262	264	334	334	334	350
71.1	68.9 68.9	68.9 68.9	68.9	6.89	68. 68. 68.	68.8	68.9	68.8	68.8	68.9
32	31 31	31	31	31	31 31	31	31	31	31	31
30 31	33 33	34 35	36	38	39 40	41	42	43	44	45

## ALIGNMENTS

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D.; Mentele, R.; Assfalg-Machleidt,
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A; Accession: B61495
                 R; Auerswald, E.A.; Roessler,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein
A; Residues: 380-389 < KAT1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein
A; Residues: 381-389 <KAT2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: A34030
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A;Map position: 3427-3427
A;Introns: 65/3; 102/3; 131/1; 188/3; 224/3; 253/1; 310/3; 346/3; 375/3; 401/3
C;Superfamily: kininogen; cystatin homology
C;Reywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; glyc
C;Reywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; glyc
C;Reywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; glyc
F;10-18/Domain: signal sequence #status predicted <ART>
F;10-18/Domain: systatin nogen [Kininogen II #status predicted <ART>
F;19-379/Product: LWW kininogen heavy chain #status predicted <ART>
F;19-379/Product: LWW kininogen heavy chain #status specimental <ARD>
F;19-375/Domain: cystatin homology <CYI>
F;264-375/Domain: cystatin homology <CYI>
F;364-375/Domain: cystatin homology <CXI>
F;381-389/Product: lysyl-bradykinin (kallidin II) #status experimental <ARD>
F;381-389/Product: bradykinin (kallidin I) #status experimental <ARD>
F;381-389/Product: bradykinin (kallidin I) #status experimental comp #status predicted
F;28-407,83-94,107-126,142-145,206-218,229-248,264-267,328-340,351-370/Disnlifide bonds:
F;48,169,205,294/Binding site: met-Lys (kallikrein) #status experimental
F;391-380/Cleavage site: Met-Lys (kallikrein) #status experimental
F;391-300/Lavage site: Met-Lys (kallikrein) #status experimental
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C; Date: 28 May-1986 #sequence_travision 28 Way-1986 #text_change 08-Dec-2000

C; Date: 28 Way-1986 #sequence_travision 28 Way-1986 #text_change 08-Dec-2000

C; Accession: A01279; A25276; S33422; A91155; A24871; A27899; A27699; A31905; A34030; S02

R; Ohkubo, I.; Kurachi, K.; Takasawa, T.; Shiokawa, H.; Sasaki, M.

Biochemistry 23, 5691-5697, 1984

A; Title: Isolation of a human cDNA for alpha-2-thiol proteinase inhibitor and its identifaterence number: A90490; MUID:85122621
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A;Residues: 1-389 <OHK>
A;Residues: 1-389 <OHK>
A;Cross-references: GB:K02566; NID:g177889
K;Takagaki, Y.; Kitamura, N.; Nakanishi, S.
J. Biol. Chem. 260, 8601-8609, 1985
A;Title: Cloning and sequence analysis of cDNAs for human high molecular weight and low
A;Reference number: A92544; MUID:85234582
A;Accession: A25276
                                                                                                                          A;Content: Branker: A92345; MUID:85234583
A;Contents: annotation; gene organization
B;Pierce, 17, 52-57, 1968
A;Title: Structural features of plasma kinins and kininogens.
A;Reference number: A91455; MUID:90255622
A;Contents: annotation; bradykinin
C;Comment: The LMW kininogen precursor is produced from the same gene as the HWW form (C;Comment: Kininogen is a cysteine proteinase inhibitor, takes part in initiation of th xyproline residue is present in the kininogen by kallikrein, is a potent vasodilator, c;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prokininogen
low molecular
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                 Nakanishi,
                                                                                           human kininogen gene and a model for its
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A;Cross-references: GB:M11437; NID:g186751; PIDN:AAB59550.1; PID:g386852
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N'Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen;
N'Contains: bradykinin (kallidin I); HMW kininogen I; HMW kininogen II;
R;Kitamura, N.; Kitagawa, H.; Fukushima, D.; Takagaki, Y.; Miyata, T.; J. Biol. Chem. 280, 8610-8617, 1985
A;Title: Structural organization of the human kininogen gene and a mode
A;Feference number: A92545; MJID:85234583
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A;Cross-references: GDB:125256; OMIM:228960
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A; Molecule type: mRNA
A; Residues: 'MSNA'.233-377 <AUE>
A; Note: differences are due to known cloning artifacts
A; Note: differences. 378-314. 1985.
Eur. J. Blochem. 152, 307-314, 1985.
A; Title: The amino acid sequence of the light chain of human high-molecular-mass kini
A; Reference number: A91153; MUID:86030270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein
A; Residues: '2', 20-380 <KELL>
R; Kellermann, J.; Lottspeich, F.; Henschen, A.; Mueller-Esterl, W.
in Kinins IV, Greenbaum, L.M., and Margolius, H.S., ed., pp.85-89, Plenum Press, New
A; Title: Amino acid sequence of the light chain of human high molecular mass kininoge
A; Reference number: A27899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein
A; Residues: 379-644 <LOT>
A; Residues: 379-644 <LOT>
A; Note: the bradykinin sequence preceding the light chain sequence was not determined
R; Kellermann, J.; Lottspeich, F.; Henschen, A.; Mueller-Esterl, W.
Eur. J. Blochem. 154, 471-478, 1986
A; Title: Completion of the primary structure of human high-molecular-mass kininogen.
A; Reference number: A24871; MUID:86108361
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A;Residues: 381-389 <MAE>
R;Sasaguri, M.; Ikeda, M.; Ideishi, M.; Arakawa, K.
Biochem. Biophys. Res. Commun. 150, 511-516, 1988
A;Title: Identification of [hydroxyproline(3)]-lysyl-bradykinin released from human p
A;Reference number: A34030; MUID:88106632
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A; Residues: 1-19;189-192;310-314;381-389 <LENI>
A; Residues: 1-19;189-192;310-314;381-389 <LENI>
R; Rato, H.; Matsumura, Y.; Maeda, H.
FEBS Lett. 232, 252-254, 1988
A; Title: Isolation and identification of hydroxyproline analogues of bradykinin in hu
A; Reference number: A61495; MUID:88211869
A; Accession: A61495;
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A;Residues: 380-389 cMIN-
K; Madda, H.; Matsumura, Y.; Kato, H.
J. Biol. Chem. 263, 16051-16054, 1988
A;Title: Purification and identification of (hydroxyprolyl(3)]bradykinin in ascitic
A;Reference number: A31905; MUID:89034061
A;Recession: A31905
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A; Residues: 380-389 <SAS>
R; Lenarcic, B.; Gabrijelcic, D.; Rozman, B.; Drobnic-Kosorok, M.; Turk, V.
Biol. Chem. Hoppe-Seyler 369, 257-261, 1988
A; Title: Human cathepsin B and cysteine proteinase inhibitors (CPIs) in inflammatory
A; Reference number: S02482; MUID:89076517
                                                                 domain 3.
FEBS Lett. 321, 93-97, 1993
A;Title: Cloning, expression and characterization of human kininogen
A;Reference number: S32422; MUID:93223854
A;Accession: S32422
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A; Molecule type: protein
A; Residues: 379-389, K', 390-407, Q', 409-644 <KEL2>
R; Residues: 379-389, K', 390-407, Q', 409-644 <KEL2>
R; Mindroiu, T.; Carretero, O.A.; Proud, D.; Walz, D.; Scicli, A.G.
Biochem. Biophys. Res. Commun. 152, 519-526, 1988
Biochem. Biophys. Res. Commun. 152, 519-526, 1988
A; Title: A new Kinin molety in human plasma kininogens.
A; Reference number: A27699; MUID:88209021
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A;Note: this peptide had Pro-383 modified to 4-hydroxyproline
A;Accession: C61495
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C; Species: Rattus norvegicus (Norway rat)
C; Species: Rattus norvegicus (Norway rat)
C; Date: 20-Jun-1989 #sequence_revision 20-Jun-1989 #text_change 15-Nov-1996
C; Date: 20-Jun-1989 #sequence_revision 20-Jun-1989 #text_change 15-Nov-1996
C; Date: 20-Jun-1989 #sequence_revision 20-Jun-1989 #text_change 15-Nov-1996
S; Rutuco-Kato, S.; Matsumoto, A.; Kitamura, N.; Nakanishi, S.
J; Biol. Chem. 260, 12054-12059, 1985
A; Title: Primary structures of the mRNAs encoding the rat precursors for bradykinin a nhibitor.
A; Reference number: A92496; MUD:86008264
A; Accession: A926055
A; Molecule type: mRNA
A; Residues: 1-433 <FURA
C; Superfamily: Kininogen; cystatin homology
C; Keywords: alternative splicing
F; 10-437.Product: K-kininogen; LMM I #status predicted <NAT>
F; 19-131.Domain: cystatin homology <CY1>
F; 142-253/Domain: cystatin homology <CY2>
F; 264-375/Domain: cystatin homology <CY2>
F; 264-375/Domain: cystatin homology <CY3>
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C; pate: 08-Mar-1998 #sequence_revision 08-Mar-1999 #text_change 15-Nov-1996
C; Accession: A25486
R; Kitagawa, H; Kitamura, N; Hayashida, H; Miyata, T; Nakanishi, S.
J. Biol. Chem. 262, 2190-2198, 1987
A; Title: Differing expression patterns and evolution of the rat kininogen gene f. A; Reference number: A92625; MUID:87137443
A; Reference number: A92625; MUID:87137443
A; Residues: 1-639 <KITT
A; Residues: 1-639 <KITT
A; Note: the authors translated the codon CAA for residue 347 as Asn
C; Superfamily: kininogen; cystatin homology
C; Reywords: alternative splicing
F; 19-639/Product: kininogen; HWM I #status predicted <AIG>F; 19-639/Product: kininogen; Cystatin homology <CX?>F; 19-631/Domain: cystatin homology <CX?>F; 19-632/Domain: cystatin homology <CX?>F; 264-375/Domain: cystatin homology <CX; 264-375/Domain: cystatin homology <CX; 264-375/Domain: cystatin homology <CX; 264-375/Domain: cystatin homology <CX; 264-275/Domain: cystatin homology <CX; 264-275
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87.5%; Pred. No. 7.5;
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Pred. No.
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N;Contains: bradykinin
C;Species: Rattus norvegicus (Norway rat)
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'-ha 7; Conserv?
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293 NNHTFYFK 300
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F:142-253/Domain: cystatin homology <CY2>
F:24-375/Domain: cystatin homology <CY2>
F:24-375/Domain: cystatin homology <CY3>
F:380-389/Product: lysyl-bradykinin (kallidin I) #status experimental <BDY>
F:380-389/Product: lysyl-bradykinin (kallidin I) #status experimental <BDY>
F:380-644/Domain: HWW kininogen light chain #status experimental <LCH>
F:380-644/Domain: HWW kininogen light chain #status experimental <CHP
F:390-644/Domain: HWW kininogen light chain #status experimental <GFF 
F:390-644/Domain: HWW kininogen light chain #status experimental <GFF 
F:390-644/Domain: HWW kininogen light chain #status experimental <GFF 
F:28-614, 83-94,107-126,142-145,206-218,229-248,264-267,328-340,351-370/Disulfide bonds: F:28-614, 83-94,107-126,142-145,206-218,229-248,264-267,328-340,351-370/Disulfide bonds: F:390-380/Cleavage site: archohydrate (Asn) (covalent) #status experimental 
F:393-390/Cleavage site: Arg-Ser (kallikrein) #status experimental 
F:393-390/Cleavage site: Arg-Ser (kallikrein) #status experimental 
F:401,333,442,546,557,571,593,688/Binding site: carbohydrate (Thr) (covalent) #status experimental 
F:577/Binding site: carbohydrate (Ser) (covalent) #status experimental
A; Molecule type: protein
A; Residues: 380-389 < KRAT3>
A; Residues: 380-389 < KRAT3>
B; Lenarciv, B.; Krasovec, M.; Ritonja, A.; Olafsson, I.; Turk, V.
R: Lenarcivation of human cystatin C and kininogen by human cathepsin D.
A; Title: Inactivation of human cystatin C and kininogen by human cathepsin D.
A; Reference number: S14303; MUID:91192133
A; Accession: S1440 th
A; Residues: 264-359, N', 361-375 < LEN2>
A; Residues: 264-359, N', 361-375 < LEN2>
B; Little. S. S.: Johnson, D. A.
Biochem. J. 307, 341-346, 1995
A; Title: Human mast, cell tryptase isoforms: separation and examination of substrate-spect on unber: S55239; MUID:95251593
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A;Title: Structural features of plasma kinins and kininogens.
A;Reference number: A91455, MUID:90255622
A;Comment: The HWW kininogen precursor and the LMW form are produced from the same gene C;Comment: Kininogen is a cysteline proteinase inhibitor, takes part in initiation of the C;Comment: The glycine/histidine/lysine-rich region of HMW kininogen light chain is impo C;Comment: The glycine/histidine/lysine-rich region of HMW kininogen light chain is impo C;Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator, in xyproline residue is present in the kininogen prior to the release of bradykinin.
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A; Residues: 431-434 <STR>
Kitamura, N.; Kitagawa, H.; Fukushima, D.; Takagaki, Y.; Miyata, T.; Nakanishi, S.
J. Biol. Chem. 260, 8610-8617, 1985
A; Title: Structural organization of the human kininogen gene and a model for its evoluti
A; Reference number: A92545; MUID:8524583
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protein R09A8.2 - Caenorhabditis elegans

hypothetical protein R09A8.2 - Cae C;Species: Caenorhabditis elegans

us-09-461-061a-1.open.rpr

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C; Superfamily: human S-phase kinase-associated protein 1A
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Best Local Similarity
Matches 6; Conserv
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161 NNATLFFK 168
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A;Molecule type: DNA
A;Residues: 1-71 <STO>
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A;Note: WTABAPM
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C;Species: Oxytricha trifallax
C;Species: Oxytricha trifallax
C;Species: Oxytricha trifallax
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
C;Accession: T31107
R;Bryan, T.M.; Sperger, J.M.; Chapman, K.B.; Cech, T.R.
Proc. Natl. Acad. Sci. U.S.A. 95, 8479-8484, 1998
A;Title: Telomerase reverse transcriptase genes in Tetrahymena thermophila and Oxytricha A;Reference number: 220985; MUID:98337940
A;Accession: T31107
A;Accessi
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000 C; Accession: T24062 R; Wilkinson, J. R; Wilkinson, J. S. Wilkinson, J. S. Wilkinson, J. S. Accession: T24062 A; Accession: T24062 A; Accession: T24062 A; Accession: T240662 A; Accession: T24062 A; Ac
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submitted to the EMBL Data Library, August 1995
A; Reference number: 219854
A; Reference number: 219854
A; Accession: T24206
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-182 <WILL>
A; Cross-references: EMBL.250755; PIDN:CAA90635.1; GSPDB:GN00028; CESP:R12H7.3
A; Experimental source: clone R12H7
A; Genetics:
A; Gene: CESP:R12H7.3
A; Gene: CESP:R12H7.3
A; Gene: CESP:R12H7.3
A; Introns: 150/3
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 08-Dec-2000
C;Accession: T24206
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Pred. No. 38;
1; Mismatches
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Pred. No. 50;
1; Mismatches
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Best Local Similarity 75.0%;
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1001 NNISFYFK 1008
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49 NESTFYFK 56
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C;Accession: B83803
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A;Title: R83650; MUID:20512582; PMID:11058132
A;Accession: B83803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AP001511; GB:BA000004; NID:g10173727; PIDN:BAB04945.1; GSPDB:GA:Experimental source: strain C-125
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A; Residues: 1-182 <KOI>
A; Coss-references: EMBL: U80037; NID:g1724111; PIDN: AAB38504.1; PID:g1724112
C; Genetics: Cy. Chihoku
                                                                                                                                                                                                                                                                              hypothetical protein BH1226 [imported] - Bacillus halodurans (strain C-125)
                                                                                                                                                                                                                                                                                                      C.Species: Bacillus halodurans
C.Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Triticum aestivum (common wheat)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 08-Oct-1999
                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C, Accession: T06978
R; Koike, M.; Takezawa, D.; Arakawa, K.; Yoshida, S.
submitted to the EMBL Data Library, November 1996
A; Reference number: Z15842
A; Accession: T06978
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Pred. No. 20;
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                       Score 35; DB
Pred. No. 13;
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75.0%;
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ilarity 85.7%;
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Query Match
Best Local Similarity 75.00,
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Gaps

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2; Length 440; Indels

DB 48;

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probable cytochrome P450 T8L23.21 [imported] - Arabidopsis thaliana probable cytochrome P450 T8L23.21 [imported] - Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thalian (mouse-ear cress)
C;Species: Arabidopsis thalian, C;Shan (C;Accession: G96611
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon (C,M.; Hughes, B.; Huizar, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, A;Authors: Hunder, J.L.; Jekhins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome i of the plant Arabidopsis.
A;Accession: G96611
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-497 <sfry
C;Genetics:
A;Genetics:
A;Genetics
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85.7%; Pred. No. 54;
tive 0; Mismatches 1; Indels
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                                                 A;Genetic code: SGC3
C;Superfamily: NADH dehydrogenase (ubiquinone) chain
C;Keywords: mitochondrion; NAD; oxidoreductase
                                                                                                                                                                                                                                                                                       0; Mismatches
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85.7%; Pred. No.
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A; Introns: 10/2; 249/3; 284/1
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Best Local Similarity
Matches 6; Conserv
                     A; Genome: mitochondrion
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238 NNALFYF 244
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C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: F86024
R;Cole, S.T.; Eiglmeler, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; HG
R; Davies, R.M.; Deviin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: F86224
A;Status: preliminary
A;Acleule type: DNA
A;Residues: 1-273 < STO>
A;Cross: references: GB:AL450380; NID:g13092504; PIDN:CAC29634.1; GSPDB:GN00147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Themnosyltransferase [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Accession: A86650
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jailion, O.; Malarme, K.; Weissenbach, J.; Ehrli
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis sa
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis sa
A;Accession: A86650
A;Accession: A86650
A;Accession: A86650
A;Cross-references: GB:AE005176; PID:g12723056; PIDN:AAK04299.1; GSPDB:GN00146
A;Cross-references: strain IL1403
C;Genetics:
A;Gene: rgpB
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C; Genetics:
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85.7%;
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1919ye hypothetical protein C49D10.1 - Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 C; Accession: T31994 R; Henkhaus, J.; Wohldmann, P.; Beck, C. submitted to the EMBL Data Library, July 1997 A; Description: The sequence of C. elegans cosmid C49D10. A; Reference number: 22108 A; Reference number: 22108 A; Reference number: 21108 A; Reference number: 21108 A; Reference number: 21108 A; Reference number: 21108 A; Residues: 1-758 < HENN A; Cross-references: EMBL:AF016665; PIDN:AAC71186.1; GSPDB:GN00020; CESP:C49D10.1 A; Experimental source: strain Bristol N2; clone C49D10 A; Gene: CESP:C49D10.1 A; Map position: 2 A; Introns: 438/2
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Search completed: July 1, 2002, 16:20:36 Job time: 200 sec

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Copyright (c) 1993 - 2000 Compugen Ltd.
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## ALIGNMENTS

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Title: Perfect score:

Run on:

Sequence:

1	SULI I S_HUMAN	KNG_HUMAN P01042; P010		DE Kininogen precursor (Alpha-2-thiol proteinase inhibitor) (Contains: DE Bradykinin). GN KNG. Homo samiens (Himan)			RX MEDLINE-85234582; PubMed-2989293;	"Cloud sequence and lysts of clouds and low molecular weight pre	Two human prekiningens."; Two human prekiningens."; T piol Chem 260.8604.1885.		RP GENE STRUCTURE. DY MEDITUE-8524583. D.: Mod-2088204.		RA Nakanishi S.; RT "Structural organization of the human kininogen gene and a model for	its evolution.";	RL J. Biol. Chem. 260:8610-8617(1985). BN [3]			-	RT its identity with low molecular weight kininogen.";	-		KX MEDLINE=860302/0; Pubmed=4034110; RA Lottspeich F., Kellermann J., Henschen A., Foertsch B.,	_	RT "The amino acid sequence of the light chain of human high-molecular-	Ent T Riochem	[2]		KX MEDLINE=90255622; PubMed=4952632; RA Dierce T V :		RL Fed. Proc. 27:52-57(1968).	RN [0]		
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	105224 segs, 38719550 residues	hits satisfying chosen parameters:	length: 0 length: 2000000000	Minimum Match 0% Maximum Match 100% Listing first 45 summaries	t_40:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES		Match Length DB ID	644 1		603	. 51	82 1	1.9 196 1 HIS5_BUCAI 1.9 239 1 H2AG MOHSE	240 1		٠.	.9 434 1 KNL2_BOVIN	444 1	619 1	901 1	901 1		1066 1	2710 1	4725 1		208 1		.7 331 1	.7 331 1 7 365 1	! !
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HWW-KININGEN PLAYS AN IMPORTANT ROLE IN BLOOD COAGULATION BY
HELPING TO POSITION OPTIMALLY PREKALLIRREIN AND FACTOR XI INXT TO
HELPING TO POSITION OPTIMALLY PREKALLIRREIN AND FACTOR XI INXT TO
EACTOR XII; (3) HWW-KININGEN INHEITS THE THROMBIN-AND PLASMIN-
INDUCED AGGREGATION OF THROMBOCYTES; (4) THE ACTIVE PEPPIDE
BRADYKININ THAT IS RELEASED FROM HWW-KININGEN SHOWS A VARIETY OF
PHYSIOLOGICAL EFFECTS: (4A) INFLEDENCE IN SMOOTH MUSCLE
CONTRACTION, (4B) INDUCTION OF HYPOTENSION, (4C) NATRIORESIS AND
DIURESIS, (4D) DECREASE IN BLOOD GLUCOSE LEVEL, (4E) IT IS A
MEDIATOR OF INFLAMMATION OF NOCICEPTORS (4E3) RELEASE OF
COTHER MEDIATORS OF INFLAMMATION (6.6. PROSTAGLANDINS), (4F) IT HAS
COTHER MEDIATORS OF INFLAMMATION (6.7. PROSTAGLANDINS), (4F) IT HAS
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COTHER MEDIATORS OF INFLAMMATION (6.7. PROSTAGLANDINS), (4F) IT HAS
COTHER MEDIATORS OF INFLAMMATION (6.7. PROSTAGLANDINS), (5)
IMDIRECTLY VIA ENDOTHELLUM-DERIVED RELEASE (6) LAW-KININOGEN IS IN CONTRAST TO HWW-KININOGEN OF INVOLVED IN BLOOD
                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license gireement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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GlyCoprotein; Plasma; Repeat; Thiol protease inhibitor; Vasodilator; Bradykinin; Blood coagulation; Inflammatory response; Signal; Alternative splicing.
SIGNAL
                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Secreted.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; HWW (SHOWN HERE) AND LAW; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: PLASMA.
PTM: BRADYKININ IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN.
                                                                                                                                                                                                                                                                                      -!- SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
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AAB59550.1; JOINED.
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PRINTS; PR00334; KININOGEN.
ProDom; PD001231; Cystatin_C_M; 1.
SWART; SW00043; CY; 3.
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InterPro; IPR003243; Cystatin_C_M.
InterPro; IPR002395; Kininogen.
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PIR; A01279; KGHUH1.
PIR; A01276; A25276.
PIR; A01280; KGHUL1.
PIR; B25276; B25276.
PIR; S02482; S02482.
SWISS-2DPAGE; P01042; HUMAN.
                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; K02566; AAA35497.1; -.
EMBL; M11437; AAB59550.1; -.
Seikagaku 56:808-808(1984)
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N-LINKED (GLCNAC...) (POTENTIAL).
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O-LINKED.
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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                                                     BRADYKININ.
KININGEN LIGHT CHAIN.
CYSTATIN-LIKE 1.
CYSTATIN-LIKE 2.
CYSTATIN-LIKE 3.
HIS-RICH (ASSOCIATED WITH CLOTTING ACTIVITY).
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MEDLINE-87137443; PubMed-3029068;
Kitagawa H., Kitamura N., Hayashida H., Miyata T., Nakanishi S.;
"Differing expression patterns and evolution of the rat kininogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GLCNAC. .) (POTENTIAL).
(GLCNAC. .) (POTENTIAL).
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(GLCNAC. .) (POTENTIAL).
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T -> I (IN REF. 1).
3132B4CBAF8FBB7E CRC64;
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KININOGEN HEAVY CHAIN.
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biol. Chem. 262:2190-2198(1987)
[2]
SEQUENCE FROM N.A. (LAW ISOFORM).
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Matches 8; Conserv
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REG STRAIN-WISTAR; TISSUE-Liver;

RA Kageyama R., Kitamura N., Okkubo H., Nakanishi S.;

A Kageyama R., Kitamura N., Okkubo H.,

A Kageyama R., Kitamura N., Okkubo H.,

A Kageyama R., Kitamura N., Okkubo H.,

Bull. Chem. 252:2345-231(1987).

J. Biol. Chem. 252:2346-231(1987).

J. Biol. Chem. 252:334(1987).

J. FUNCTION: (1) KININOGENS MEE INHIEITORS OF THIOL PROTEASES; (2)

HWA-KININOGEN PLAYS AN IMPORTANT ROLE IN BLOOD COAGULATION BY

CC HELPING TO POSITION OF THANDERS OF THE ACTIVE PEPTIDE

RACTOR XII; (3) HWW-KININOGEN INHIEITS THE THROMBIN-AND PLASMIN-

CC FACTOR XII; (3) HWW-KININOGEN WINIBIRTS THE TRROMBIN-AND PLASMIN-

CC FACTOR XII; (3) HWW-KININOGEN WINIBIRTS THE ACTIVE PEPTIDE

BRADYKININ THAT IS RELEASED FROM HWW-KININOGEN SHOWS A VARIETY

CC COMTRACTION, (4B) INDUCTION OF HYPOTENSION, (4C) NARRIURESIS AND

DIURESIS, (4D) DECREASE IN BLOOD GLUCOSE LEVEL, (4E) IT IS A

MEDIATOR OF INFLAMMATION OF UNCICEPTORS (4E3) RELEASE OF

OTHER MEDIATORS OF INFLAMMATION OF ONCICEPTORS (4E3) RELEASE OF

CTHER MEDIATORS OF INFLAMMATION OF ONCICEPTORS (4E3) RELEASE OF

CHER MEDIATORS OF INFLAMMATION OF PROSTAGLANDINS), (4F) IT HAS

CC RIMINOGEN IS IN CONTRAST TO HWW-KININOGEN NOT INVOLVED IN BLOOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- SUBCELLULAR LOCATION: Secreted.
-i- ALTERNATIVE PRODUCTS: 2 ISOFORMS; HWW (SHOWN HERE) AND LAW; ARE PRODUCED BY ALTERNATIVE SPLICING.
-i- TISSUE SPECIFICITY: PLASAED FROM KININGEN BY PLASMA KALLIKREIN.
-i- PTM: BRADYKININ IS RELASED FROM KININGEN BY PLASMA KALLIKREIN.
-i- MISCELLANEGUS: RAT EXPRESS FOUR TYPES OF KININGGENS: THE CLASSICAL HWW/LMW KININGGENS AND TWO ADDITIONAL LAW-LIKE KININGGENS: T-I AND
                                                                                                                                                                                                                                Fung W.-P., Schreiber G.; "Structure and expression of the genes for major acute phase alpha 1-protein (thiostatin) and kininogen in the rat."; The statem 262:9298-9308(1987).
                    Furuto-Kato S., Matsumoto A., Kitamura N., Nakanishi S.;
Prihany structures of the mRNAs encoding the rat precursors for
bradykinin and T-kinin. Structural relationship of kininogens with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biol. Chem. 260:12054-12059(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M14369; AAA41484.1; -.
EMBL; M14369; AAA41485.1; ALT_SEQ.
EMBL; M16455; AAA41482.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00334; KININOGEN.
ProDom; PD001231; Cystatin_C_M; 1.
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InterPro; IPR003243; Cystatin_C_M.
InterPro; IPR002395; Kininogen.
                                                                                                                                                                                        STRAIN-BUFFALO;
MEDLINE-87250580; Pubmed-2439509;
MEDLINE=86008264; PubMed=2413018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L29428; AAA41486.1; -. EMBL; M11884; AAA41487.1; -.
                                                                                                                            J. Biol. Chem. 260:12054-1
[3]
SEQUENCE OF 1-65 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-41 FROM N.A.
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SMART; SM00043; CY; 3.
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PIR; A28055; A28055.
HSSP; P01040; 1DVD.
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                                                                                                    inhibitor
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BYAN T. Sperger LDAGE CONTROL OF THE STATE O
             Glycoprotein; Plasma; Repeat; Thiol protease inhibitor; Vasodilator; Bradykinin; Blood coagulation; Inflammatory response; Signal; Alternative splicing; Multigene family.
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic subunit) (Telomerase subunit P133).
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Eukaryota; Alveolata; Ciliophora; hypotrichs; Stichotrichida;
Oxytrichidae; Oxytricha.
NCBI_TaxID=5946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 39; DB 1; Length 639;
Pred. No. 3.3;
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INTERCHAIN (BY SIMILARITY).
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D3172DF94FF56AF5 CRC64;
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CYSTATIN-LIKE 2.
CYSTATIN-LIKE 3.
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KININOGEN HEAVY CHAIN
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PS00287; CYSTATIN; 2.
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Best Local Similarity 87.5-
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P35672;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-90380429; PubMed-2400605; Rachinsky T.L., Camp S., Li Y., Ekstroem T.J., Newton M., Taylor P.; "Molecular Cloning of mouse acetylcholinesterase: tissue distribution of alternatively spliced mRNA species."; Newton 5:317-327(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- MISCELLANDOUS: CHOLINESTERASE IS HIGHLY REACTIVE WITH ORGANOPHOSPHATE ESTERS.
-!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                  PRINTS; PR01365; TELOMERASERT.
Transferase; RNA-directed DNA polymerase; Telomere; Nuclear protein;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-CT-1993 (Rel. 27, Last sequence update)
Li>5.UUL-1998 (Rel. 36, Last annotation update)
Cholinesterase precursor (EC 3.1.1.8) (Acylcholine acylhydrolase)
(Choline esterase II) (Butyrylcholine esterase)
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"Use of the polymerase chain reaction for homology probing of butyrylcholinesterase from several vertebrates.";
J. Biol. Chem. 266:6966-6974(1991).
-:- CATALYTIC A. An acylcholine + H(2)O = choline + a carboxylic acid anion.
                                                                                                                                                                                                                                                                                                                                                                                                     Score 36; DB 1; Length 1132;
Pred. No. 22;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                        1132 AA; 134124 MW; 81E145F5F24392DC CRC64;
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                                                                                                                                                                                                                          EMBL; AF060230; AAC39163.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                        80.0%;
75.0%;
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  TELOMERASE SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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15-JUL-1998
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SEQUENCE
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Q03311;
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Best Local (
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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INTERCHAIN (BY SIMILARITY).

N-LINKED (GLCNAC. ..) (POTENTIAL).

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MEDLINE-95089692; PubMed-7997169;
Kaniga K., Bossio J.C., Galan J.E.;
"The Salmonella typhimurium invasion genes invF and invG encode
homologues of the AraC and PulD family of proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . .) (POTENTIAL)
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Pred. No. 44;
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01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                            InterPro: IPR002018; Carboxylesterase_B.
InterPro: IPR000997; Cholinesterase.
InterPro: IPR000379; Est_lip_thioest_actsite.
Pfan, PF00135; Coesterase; 1.
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                                                                                                                                                                                                                                                                                    PRINTS; PRO0878; CHOLNESTRASE.
PROSITE: PSO0122; CARBOXXLESTERASE_B_1; 1.
PROSITE: PSO0941; CARBOXXLESTERASE_B_2; 1.
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85.7%;
                                                                            EMBL; M99492; AAA37328.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella typhimurium.
                                                                                                                                HSSP; P21836; 1MAH.
MGD; MGI:894278; Bche.
                                                                                                        PIR; A39768; A39768.
HSSP; P21836; 1MAH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 6; Conserv
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SEQUENCE FROM N.A.
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Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                       STRAIN-LT2 / SGSC1412 / ATCC 700720;
MEDLINE-LT2 / SGSC1412 / ATCC 700720;
MEDLINE-LT34948; PubMed=11677609;
McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
"Complete genome sequence of Salmonella enterica serovar Typhimurium LT2":
                                                                                                                                Nature 413:852-856(2001).
-!- FUNCTION: INVOLVED IN THE INVASION OF THE CELLS OF THE INTESTINAL
EPITHELIUM. COULD BE NECESSARY FOR THE EXPORT OF INVASION RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RPVLLTQENVP -> APGITSSGKCS (IN REF. 2).
8022905BE256058D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR01337; TYPE30MGPROT.
PROSITE; PS00875; T2SP_D; 1.
Virulence: Transport; Protein transport; Signal; Outer membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  INVG PROTEIN.

A -> R (IN REF. 2).

E -> Q (IN REF. 2).

LRDGKWIP -> CAIRKWLER (IN REF. 2).

AMPAFSANG -> RCQRFQRM (IN REF. 2).

G -> S (IN REF. 2).

AAA -> KPAEQ (IN REF. 2).

A -> T (IN REF. 1).

I -> V (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .<u>`</u>
                                                                                                                                                                             -i- SUBCELLULAR LOCATION: Outer membrane (Potential).
-i- SIMILARITY: BELONGS TO THE PULD/OUTD/EXED/XPSD FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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01-NOV-1991 (Rel. 20, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
GCN2 in kinase GCN2 (EC 2.7.1.-).
GCN2 OR AASI OR YDR283C.
Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1590 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71.1%; Score 32; 75.0%; Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                         EMBL; AE008832; AAL21778.; PIR; S38422; S38422.
StyGene; SG10188; invG.
InterPro; IPR000016; Bac_GSPprotein.
InterPro; IPR003522; SecIII_OMPG.
Pfam; PF00263; GSPII_III; 1.
Microbiol. 13:555-568(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61765 MW;
                                                                                                                                                                                                                                                                                                     EMBL; X75302; CAA53049.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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562
12
121
205
240
243
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Matches 6; Conserv
                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome
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GCN2_YEAST
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TO 364 AND FROM POSITION 981 ONWARD DUE TO FRAMESHIFTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- FUNCTION: STIMULATES GCN4 TRANSLATION IN AMINO ACID-STARVED CELLS
BY PHOSPHORYLATING THE ALPHA SUBUNIT OF EIF-2 (SUI2) ON SER-52.
-!- SUBCELLULAR LOCATION: ASSOCIATES WITH THE 60S SUBUNIT OF
SEQUENCE FROM N.A.
MEDLINE-89282814; Pubmed-2660141;
MEDLINE-89282814; Pubmed-2660141;
WER R.C., Jackson B.M., Hinnebusch A.G.;
"Juxtaposition of domains homologous to protein kinases and histidyltraposition of domains homologous to protein kinases that RNA synthetases in GCN2 protein suggests a mechanism for coupling GCN4 expression to amino acid availability.";
Proc. Natl. Acad. Sci. U.S.A. 86:4579-4583(1989).
                                                                                                                                                                                                                                                                                                                                                                       STRAIN-S288C;
MEDIINE-88251291; PubMed-3290651;
Roussou I., Thireos G., Hauge B.M.;
"Transcriptional-translational regulatory circuit in Saccharomyces cerevisiae which involves the GCN4 transcriptional activator and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Phosphorylation of initiation factor 2 alpha by protein kinase GCN2 mediates gene-specific translational control of GCN4 in yeast."; Cell 68:585-596(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIBOSOMES.
-!- INDUCTION: BY AMINO ACID STARVATION AND IN THE PRESENCE OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. GCN2 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ramirez M., Wek R.C., Hinnebusch A.G.;
"Ribosome association of GCN2 protein kinase, a translational
activator of the GCN4 gene of Saccharomyces cerevisiae.";
Mol. Cell. Biol. 11:3027-3036(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTIVITY ON SUI2.
MEDLINE-92154672; Pubmed-1739968;
Dever T.E., Feng L., Wek R.C., Cigan A.M., Donahue T.D.,
Hinnebusch A.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; S05781; OKBYN2.
PIR; A27723; A27723.
HSSP: P24941; JUST.
SGD; S0002601; GCN2.
InterPro; IPR002106; AA_tRNA_ligase_II.
InterPro; IPR002106; Buk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
PROSITE; PS00039; PA_TRNA_LIGASE_II_2; UNKNOWN_I.
PROSITE; PS001007; PROTEIN_KINASE_ATP; 1.
PROSITE; PS001108; PROTEIN_KINASE_ST; 1.
PROSITE; PS001108; PROTEIN_KINASE_ST; 1.
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EMBL; M20487; AAA34881.1; ALT_FRAME.
EMBL; U51030; AAB64461.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCN2 protein kinase.";
Mol. Cell. Biol. 8:2132-2139(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-91246169; PubMed-2038314;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-S288C / AB972;
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96882458044823A8 CRC64;

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EMBL; F14757; CAA23231.1; -.
InterPro; IPR006571; Zf-CCCH.
Pfam; PF00642; zf-CCCH; 1.
Nuclear protein; RNA-binding; mRNA splicing; Zinc-finger; Repeat.
                                                                                    82
9416 MW;
                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                            STANDARD;
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180
                                                                                                                                                                                                                                                                                                                                                                            symbiotic bacterium)
                                                                                    82
82 AA;
                                                                                                                                                 Similarity 5; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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ACT_SITE 77
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17 NCSFYFK 23
                                                                                                                                                                                       NATFYFK 8
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SEQUENCE
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ACT_SITE
SEQUENCE
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Best Local
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HISS_BUCAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mamm. Genome 7:509-517(1996).

-! FUNCTION: PLAKS A CRITICAL ROLE IN BOTH CONSTITUTIVE AND ENHANCER-DEPENDENT SPLICING BY MEDIATING ESSENTIAL PROTEIN-PROTEIN INTERACTIONS AND PROTEIN-RNA INTERACTIONS REQUIRED FOR ACCURATE 3' SPLICE SITE SELECTION. DIRECTLY MEDIATES INTERACTIONS BETWEEN UZAF65 (LARGE SUBUNIT) AND PROTEINS BOUND TO THE ENHANCERS AND THUS MAY FUNCTION AS A BRIDGE BETWEEN UZAF65 AND THE SHHANCER COMPLEX TO RECRUIT IT TO THE ADJACENT INTRON (BY SIMILARITY).
-! SUBUNIT: ASSOCIATES WITH A 65 kDa PROTEIN.
-! SUBCELLULAR LOCATION: NUCLEAR.
-! SUBCELLULAR LOCATION: NUCLEAR.
-! SIMILARITY: CONTAINS IN RECOGNITION MOTIF (RRM).
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Small intestine;
MEDLINE=96327607; PubMed=8672129;
Winterce A.K., Fredholm M., Davies W.;
Winterio and Characterization of a porcine small intestine cDNA library: analysis of 839 clones.";
Mamm. Genome 7:509-517(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                          TIKAKLP -> NYKGKIA (IN REF. 2).
LMSSEMMEN -> YVFSNHGKS (IN REF. 2).
I -> M (IN REF. 2).
P -> A (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-WAR-2002 (Rel. 41, Last annotation update)
Splicing factor UZAF 35 kpa subunit (UZ auxiliary factor 35 kpa subunit) (UZ snRNP auxiliary factor small subunit) (Fragment).
                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                              RSRYASDFEEIAVL -> DHDMLLTLKRLHFS
                       Amino-acid biosynthesis; Aminoacyl-tRNA synthetase; Repeat.

DOMAIN 187 458 PROTEIN KINASE 1.

DOMAIN 530 912 PROTEIN KINASE 2.
                                                                                                                                                                                                                                                                                      Length 1590;
                                                           HISTIDYL-TRNA SYNTHETASE LIKE
                                                                                                                                                                      (IN REF. 2).
S -> T (IN REF. 2).
IL -> M (IN REF. 2).
F -> C (IN REF. 2).
M -> K (IN REF. 2).
E -> Q (IN REF. 2).
My, 768815424F64FIAA CRC64;
           Serine/threonine-protein kinase; ATP-binding;
                                                                      ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                      Score 32; DB 1; I
Pred. No. 1.8e+02;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                           82 AA.
                                                                                                                                                                                                                                                  182041 MW;
                                                                                                                                                                                                                                                                                      71.18;
75.08;
                                                                                                                                                                                                                                                                                                               Conservative
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406
520
536
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658 65
770 77
885 88
                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
6, Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                             266 NNATEVWK 273
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                                                                                                                                                                                                                                                                                                                                     1 NNATFYFK 8
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          Transferase:
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ID U2AG_PIG
AC Q29350;
                                                                                               ACT_SITE
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shigenobu S., Watenabe H., Hattori M., Sakaki Y., Ishikawa H.;
Shigenobu S., Watenabe H., Hattori M., Sakaki Y., Ishikawa H.;
"Genome sequence of the endocellular bacterial symbiont of aphids
Buchnera sp. Aps."

Nature 407:81-86(2000).

-I-FUNCTION: CATALYZES AN AMIDOTRANSFERASE REACTION THAT GENERATES
IMDAZOLE-GIVEEROL PHOSPHATE AND S-AMINOIMIDAZOL-4-CARBOXAMIDE
RIBONUCLEOTIDE, WHICH IS USED FOR PURINE SYMTHESIS.

-I-PATHWAY: FIFTH STEP IN HISTIDINE BIOSYNTHETIC PATHWAY.

-I-SOMCELLULAR LOCATION: CYLOPIASMIC (PRODABLE).

-I-SIMILARITY: BELONGS TO THE HISH FAMILY.

-I-SIMILARITY: CONTAINS 1 TYPE-1 GLUTAMINE AMIDOTRANSFERASE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Length 82;
                                                         1; Indels
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SIMILARITY.
904624B74BBEBE5D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proteobacteria; gamma subdivision; Buchnera
DB 1;
14;
                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Amidotransferase hisH (EC 2.4.2.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 34;
                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 31; DB Pred. No. 34; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00442; GATASE_TYPE_I; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY
Score 31;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-20445173; PubMed-10993077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY
BY
BY
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InterPro; IPR000991; GATase_1.
Pfam; PF00117; GATase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21679 MW;
68.9%;
71.4%;
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Similarity 71.4%;
5; Conservative 1
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STAIN=C57BL/6J; TISSUE-Small intestine;

XX MEDINE-210B5660; PubMed=11217851;

XX Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arawawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arawawa T., Hara A., Shibata K., Xiyosawa H., Kondo S., Yamanaka I.,

Alzawa M., Isawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Caavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Caavant T.,

Radota K., Matsuda H.P., Sulvi R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baddarelli R., Barsh G.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Radotone P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakanoto N.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakanoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Winshaw-Boolis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nasabilani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Functional annotation of a full-length mouse cDNA collection.";
                                                                                            .UZAG_MOUSE STANDARD, PRT; 239 AA.
Q9D883; Q9C298; Q99LX2;
Q1-MAR-2002 (Rel. 41, Created)
Q1-MAR-2002 (Rel. 41, Last sequence update)
Q1-MAR-2002 (Rel. 41, Last annotation update)
Splicing factor UZAF 35 kDa subunit (UZ auxiliary factor 35 kDa subunit) (UZ snRNP auxiliary factor small subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THE U2AF35/U2AF65 HEPERODIMER (By Similarity).
--- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
--- SIMILARITY: CONTAINS 2 C3H1-TYPE ZINC FINGERS.
--- SIMILARITY: BELONGS TO THE SR FAMILY OF SPLICING FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AK008332; BAB25609.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 2-239 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Breast tumor;
            135 NNSREYF 141
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                                                                              U2AG_MOUSE
                                                               RESULT
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MEDLINE-202879; PubMed-10830953; Matanabe H., Yada T., MEDLINE-2028799; PubMed-10830953; Matanabe H., Yada T., Paylor T.D., Watanabe H., Yada T., Park H.-S., Toyoda A., Taylor T.D., Watanabe H., Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A., Menzel U., Dalbabar J., Kumpf K., Lehmann R., Patterson D., Reichwald K., Rump A., Schillabel M., Schudy A., Zimmermann W., Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S., Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E., Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P., Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H., Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E., Rehreneyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
8plicing factor U2AF 35 kDa subunit (UZ auxiliary factor 35 kDa subunit) (UZ snRNP auxiliary factor small subunit).
U2AF1 OR U2AF35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Fetal brain;
MEDLINE=92409598; PubMed=1388271;
Zhang M., Zamcore P.D., Carmo-Fonseca M., Lamond A.I., Green M.R.
"Cloning and intracellular localization of the U2 small nuclear ribonucleoprotein auxiliary factor small subunit.";
Proc. Natl. Acad. Sci. U.S.A. 89:8769-8773(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                   Score 31; DB 1; Length 239;
Pred. No. 41;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                           ARG/GLY/SER-RICH (RS DOMAIN).
G -> R (IN REF. 1; BAB25609).
DFF944210581244D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND SEQUENCE OF 68-89 AND 126-151.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lehrach H., Reinhardt R., Yaspo M.-L.;
"The DNA sequence of human chromosome 21.";
Nature 405:311-319(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-96249383; PubMed-8647433;
                              MGD; MGI:9884; UZGfI.
InterPro; IPR000504; RRM.
InterPro; IPR0005954; RRM.
InterPro; IPR0005954; RRM_I.
Pfam; PF00076; rrm; 1.
Fram; PF00642; zf-CCCH; 2.
SMART; SM00360; RRM; 1.
SMART; SM00361; RRM_I; 1.
                                                                                                                                                                                                                                                                            65 147 RN
149 173 C3
179 238 AI
187 281 G
239 AA; 27815 MW;
BAB28511.1; -. AAH02184.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                       68.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                          ZN_FING
DOMAIN
CONFLICT
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The splicing factor U2AF35 mediates critical protein-protein are splicing factor U2AF35 mediates critical protein-protein are splicing factor U2AF35 mediates critical protein-protein interactions in constitutive and enhancer-dependent splicing.";

AL Genes Dev. 10:1356-1368(1996).

CI FUNCTION: PLAKS A CRITICAL ROLE IN BOTH CONSTITUTIVE AND ENHANCER-DEPENDENT SPLICING BY MEDIATING ESSENTIAL PROTEIN-PROTEIN AND FORTEN-PROTEIN PROTEIN-PROTEIN FOR ACCUBATE 3' SPLICE SITE SELECTION. DIRECTLY MEDIATES INTERACTIONS BETWEEN U2AF65 (LARGE SUBGURIT), AND PROTEINS BOUND TO THE ENHANCER AND THUS MAY FUNCTION AS A BRIDGE BETWEEN U2AF65 AND THE ENHANCER COMPLEX TO RECRUIT IT TO THE ADJACENT INTRON.

CISCUMPLEX TO RECRUIT IT TO THE ADJACENT INTRON.

CISCUMPLEX TO RECRUIT IT A 65 KDB PROTEIN.

CISCUMPLEX TO RECRUIT IN A 65 KDB PROTEIN.

CISCUMPLEX AND THE CARBOXY-TERMINAL DOMAIN IS REQUIRED FOR FORMATION OF TRAZ, AND THE CARBOXY-TERMINAL DOMAIN IS REQUIRED FOR FORMATION OF TRAZ, AND THE CARBOXY-TERMINAL DOMAIN IS REQUIRED FOR FORMATION OF TRAZ, AND THE CARBOXY-TERMINAL DOMAIN IS REQUIRED FOR FORMATION OF TRAZ INTRATIY: CONTAINS 1 RNA RECOGNITION WOTIF (RRM).

CI-SIMILARITY: BELONGS TO THE ST FAMILY OF SPLICING FACTORS.
                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send-an email to license@isb-sib.ch).
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Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR005504; RRM.
InterPro; IPR000571; 2f-CCCH.
Pfam; PF00076; rrm; 1.
Pfam; PF00642; zf-CCCH; 2.
SMART; SM00356; RRM; 1.
SMART; SM00356; ZnF_C3H1; 2.
PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM_RNP_1; FALSE_NEG.
Nuclear protein; RNA binding; RNA splicing; Zinc-finger; Repeat.
ZN_FING 13 41 C3H1-TYPE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    094535; Q9VPN4;
01.NOV-1997 (Rel. 35, Created)
16.0CT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Splicing factor U2af 38 kDa subunit (U2 auxiliary factor 38 kDa subunit) (U2 SNRNP auxiliary factor small subunit).
U2AF38 OR CG3582.
Drosophila melanogaster (Fruit fly).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68.9%; Score 31; DB 1; Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3DA130DCE0B953F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNA-BINDING (RRM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 42;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27872 MW;
                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M96982; AAA36619.1; --
EMBL; AP001748; BAA95534.1; --
PIR; 827969; 827969.
PIR; A46179; A46179.
MIM; 191317; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173
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Matches 5; Conserva
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149
178
210
240 AA;
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U2AG_DROME
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SEQUENCE FROM N.A.
STRAIN=EL TOR N16961 / SEROTYPE 01;
     product.";
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Best Local Similarity
Matches 6; Conserv
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109 NDATFYEK 116
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  SOUR THE TENT OF T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=K12;
MEDLINE=92202162; PubMed=1551850;
Meinnel T., Schmitt E., Mechulam Y., Blanquet S.;
"Structural and biochemical characterization of the Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38) (AGPR) (N-acetyl-galutamate semialdehyde dehydrogenase) (NAGSA dehydrogenase).
ARGC OR B3958.
     InterPro; IPROUUS).1.

Pfam; PF00076; rrm; 1.

Pfam; PF00642; zf-CCCH; 2.

SWART; SW00361; RRM_1; 1.

SWART; SW00356; ZnE_C3H1; 2.

PROSITE; PS00030; RRM_RNP_1; PALSE_NEG.

Nuclear protein; RNA-binding; mRNA-binding; mRNA-bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-80121510; PubMed-2851495;
Parsot C., Boyen A., Cohen G.N., Glansdorff N.;
Nucleotide sequence of Escherichia coli argB and argC genes:
comparison of N-acetylglutamate kinase and
N-acetylglutamate-gamma-semialdehyde dehydrogenase with homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Analysis of the Escherichia coli genome. IV. DNA sequence of the region from 89.2 to 92.8 minutes.";
Nucleic Acids Res. 21:5408-5417(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 264;
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MEDLINE-94089392; PubMed-8265357;
Blattner F.R., Burland V.D., Plunkett G. III, Sofia H.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                            H -> D (IN REF. 1).
577285FB66FDB2F5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 31;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic Acids Res. 10:8031-8048(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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InterPro; IPR003954; RRM_1.
InterPro; IPR000571; Zf-CCCH.
                                                                                                                                                                                                                                                                                                                                                                                         29877 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68.98;
71.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene 68:275-283(1988).
                                                                                                                                                                                                                                                                                                                                                                                      264 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 5; Conserv
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CONFLICT
SEQUENCE
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"J. Bacteriol. 174:2323-2331(1992).
-!- CATALYTIC ACTIVITY: N-acetyl-L-glutamate 5-semialdehyde + NADP(+)
-+ Phosphate = N-acetyl-5-glutamyl phosphate + NADPH.
-+ PATHWAY: THIRD STEP IN ARGININE BLOSYNTHESIS.
-!- SATHWAY: THIRD STEP TO THE NAGSA DEHYDROGENASE FAMILY.
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MEDLINE-97101069; PubMed-8945596;
Sperandio V., Bailey C.C., Giron J.A., Dirita V.J., Silveira W.D.,
Vettore A.L., Kaper J.B.;
Cloning and characterization of the gene encoding the OmpU outer
membrane protein of Vibrio cholerae.";
Infect. Immun. 64:5406-5409(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arginine biosynthesis; Oxidoreductase; NADP; Complete proteome. ACT_SITE 154 154 BY SIMILARITY. SEQUENCE 334 AA; 35952 MW; 67AC195ECE1C4789 CRC64;
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Cloling and expression of ompU of Vibrio cholerae and its
antigenicity analysis.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68.9%; Score 31; DB 1; Length 334; 75.0%; Pred. No. 58; 1; Indels ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Outer membrane protein U precursor (Porin ompU).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; JT0332; RDECEP.
ECGGENE; EG10065; argC.
InterPro; IPR000706; AGPR_act_site.
InterPro; IPR000534; Semialdh_dh.
Pfam; PF02118; Semialdhyde dh; 1.
Pfam; PF02774; Semialdhyde_dhc; 1.
ProDom; PD003765; AGPR_act_site; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; J01587; AAB59146.1; --
EMBL; X55417; --; NOT_ANNOTATED_CDS.
EMBL; U00006; AAC43064.1; --
EMBL; AE000470; AAC76940.1; --
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SM00043; CY;
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434 AA;
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Best Local Similarity
Matches 5; Conserv
                         chain portion.";
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CARBOHYD
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PEPTIDE
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DOMAIN
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                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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       Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L., Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A., Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D., Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P., McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                 -!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-83117859; PubMed=6572010;
Nawa H., Kitamura N., Hirose T., Asai M., Inayama S., Nakanishi S.;
"Primary structures of bovine liver low molecular weight kininogen
precursors and their two mRNAs.";
Proc. Natl. Acad. Sci. U.S.A. 80:90-94(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Kininogen, LMW II precursor (Thiol proteinase inhibitor) [Contains:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus (Bovine).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                              "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                              Transmembrane; Porin; Signal; Outer membrane; Complete proteome. SIGNAL 1 21 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 19-376.
BEDLINE-87137530; Pubmed-3546295;
Sueyoshi T., Miyata T., Hashimoto N., Kato H., Hayashida H.,
Miyata T., Iwanaga S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             3 -> AS (IN REF. 1).
CECB39070E441732 CRC64;
                                                                                                                                                                                                                                                                                                                                                                          OUTER MEMBRANE PROTEIN U.
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E -> K (IN REF. 1).
VG -> AS (IN REF. 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 31;
Pred. No. 5
                                                                                                                                                                                                                                                            EMBL; AF253529; AAF64526.1; --
EMBL; AE004149; AAF93799.1; ALT_INIT.
TIGR; VC0633; --
                                                                                                                                                                                                                                                                                            Tick; vcvss,
Interpro; IPR001702; Gram_neg_porin.
Interpro; IPR003229; OMP_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
MEDLINE=20406833; PubMed=10952301;
                                                                                                                                                                                                                                                                                                                        Pfam; PF00267; Gram-ve_porins; 1.
Probom; PD000808; OMP_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                          36645 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          68.9%;
71.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                   Nature 406:477-483(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                       341 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :||:||!
299 DATYYFK 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                         cholerae
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KNL2_BOVIN
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                                                                                             1. J. Blol. Chem. 262:2768-2779(1987).

1. J. Blol. Chem. 262:2768-2779(1987).

1. J. Blol. Chem. 262:2768-2779(1987).

1. J. Blol. Chem. 262:2768-2779(1987).

1. J. Blol. Chem. 262:2768-2779(1987).

1. J. Blol. Chem. 262:2768-2779(1987).

2. LWALTON: (1) KININOGENS ARE INHIBERSED FROM LAW-KININOGEN SHOWS AVAILTERS OF PHYSIOLOGICAL EFFECTS: (3A) INFLUENCE IN SMOOTH MUSCAL CONTRACTION, (3B) INNOCTION OF HYPOTENSION, (3C)

2. SUBCELLULAR LOCATION: EXTRACHILL RESULT OF ALFERNATE MRNA SPLICING. THE SEQUENCES OF BOTH KININOGENS ARE INCOMPLES AND GENE AS THE RESULT OF ALFERNATE WEND SPLICING. THE SEQUENCES OF BOTH KININOGENS ARE IDENTICAL UP TO RESIDUE 399.

2. C. TO RESIDUE 399.

3. C. TO RESIDUE 399.

4. MINCHENSIANIN IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN.

4. MINCHENSIANIN IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN.

5. TO RESIDUE 399.
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"Bovine high molecular weight kininogen. The amino acid sequence, positions of carbohydrate chains and disulfide bridges in the heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00287; CYSTATIN; 2.
Glycoprotein; Plasma; Repeat; Vasodilator; Alternative splicing;
Thiol protease inhibitor; Bradykinin; Signal.
SIGNAL
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CYSTATIN-LIKE 1.

CYSTATIN-LIKE 2.

CYSTATIN-LIKE 2.

CYSTATIN-LIKE 2.

CYSTATIN-LIKE 3.

PYRROLIDOME CARBOXYLIC ACID.

N-LINKED (GLCNAC. . .).

N-LINKED (GLCNAC. . .); OR 169.

N-LINKED (GLCNAC. . .) (PARTIAL).

N-LINKED (GLCNAC. . .)

N-LINKED (GLCNAC. . .)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KININOGEN, LAW II.
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Pred. No. 76;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HEAVY CHAIN.
BRADYKININ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERCHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; V00427; CAA23710.1; -.
PIR; A01284; KGBOL2.
HSSP; P01038; 1A90.
InterPro; IPR000010; Cystatin.
InterPro; IPR00343; Cystatin_C_M.
Pfam; PP00031; Cystatin, 3.
ProDom; PD001231; Cystatin_C_M.
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ilarity 62.5%;
Conservative
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VARIANT PLA2G7 DEFICIENCY ARG-281.
MEDLINE=97396177; PubMed=9245731;
Yamada Y., Yokota M.;
"Loss of activity of plasma platelet-activating factor acetylhydrolase due to a novel Gln281-->Asm mutation.";
                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NAR-2002 (Rel. 31, Last annotation update)
Platelet-activating factor acetylhydrolase precursor (EC 3.1.1.47)
(PAF acetylhydrolase) (PAF 2-acylhydrolase) (LDL-associated phospholipase A2) (LDL-PLA(2)) (2-acetyl-1-alkylglycerophosphocholine esterase) (1-alkyl-2-acetylglycerophosphocholine esterase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Purification, properties, sequencing, and cloning of a lipoprotein-associated, serine-dependent phospholipase involved in the oxidative modification of low-density lipoproteins "; Arterioscler. Thromb. Vasc. Biol. 16:591-599(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-96259525; PubMed-8675689;
Stafforini D.M., Satoh K., Atkinson D.L., Tjoelker L.W.,
Eberhardt C., Yoshida H., Imaizumi T., Takamatsu S., Zimmerman G.A.,
McIntyre T.M., Gray P.W., Prescott S.M.;
"Platelet-activating factor acetylhydrolase deficiency. A missense
mutation near the active site of an anti-inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dietsch G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-96197208; PubMed-8624782; Tew D.G., Southan C., Rice S.Q.J., Lawrence M.P., Li H., Boyd H.F., Moores K., Gloger I.S., Macphee C.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Myeloid;
MEDIARE-85214779; PubMed-7700381;
Tjoelker L.W., Wilder C., Eberhardt C., Stafforini D.M., Dietsch G Schimpf B., Hooper S., le Trong H., Cousens L.S., Zimmerman G.A., Yamada Y., McIntyre T.M., Prescott S.M., Gray P.W.;
"Anti-inflammatory properties of a platelet-activating factor acetylhydrolase.",
                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
VCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hiramoto M., Yoshida H., Imaizumi T., Yoshimizu N., Satoh K.;
"A mutation in plasma platelet-activating factor acetylhydrolase (Val279-->Phe) is a genetic risk factor for stroke.";
Stroke 28:2417-2420(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Plasma platelet-activating factor acetylhydrolase is a secreted phospholipase A2 with a catalytic triad."; J. Biol. Chem. 270:25481-25487(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tjoelker L.W., Eberhardt C., Unger J., le Trong H., Zimmerman G.A., McIntyre T.W., Stafforini D.W., Prescott S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. Biophys. Res. Commun. 236:772-775(1997).
                                                                                                                   441 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND SEQUENCE OF 42-57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clin. Invest. 97:2784-2791(1996).
                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-98074100; PubMed-9412624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 374:549-553(1995).
                                                                                                                   STANDARD;
290 HDGTFYFK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT PHE-279.
                                                                                                              PAFA_HUMAN 8
013093; 015692;
01-NOV-1997 (Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                phospholipase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANT PHE-279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gray P.W.;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The Ile198Thr and Ala379Val variants of plasmatic PAF-acetylhydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF) BY HYDROLYZING THE SN-2 ESPER BOND TO YIELD THE BIOLOGICALLY INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANTS HIS-92; THR-198 AND ALA-379.
MEDLINE-20311534; PubMed-10733466;
Kruse S., Mao X.-O., Heinzmann A., Blattmann S., Roberts M.H.,
Braun S., Gao P.-S., Forster J., Kuehr J., Hopkin J.M., Shirakawa T.,
Deichmann K.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- CATALYTIC ACTIVITY: 2-acetyl-1-alkyl-sn-glycero-3-phosphocholine H(2)O = 1-alkyl-sn-glycero-3-phosphocholine + acetate.
-i- SUBCELLIDAR LOCATION: Extracellular.
-i- TISSUE SPECIFICITY: PLASMA.
-i- POLYMORPHISM: THE POLYMORPHIC ALLELES THR-198 AND VAL-379 ARE
                                                                                                                                                                                                                                                                                                                                                                                                            not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASSOCIATED WITH ATOPY AND ASTHMA.
DISEASE: DEFECTS IN PLA2G7 ARE THE CAUSE OF PLA2G7 DEFICIENCY A
DISEASE: DEFECTS IN PLA2G7 ARE THE CAUSE OF PLA2G7 DEFICIENCY A
DISEASE: DEFECT IN THE PRESENCE OF INFLAMMATORY
BODILY RESPONSES
SIMILARITY: PRATIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,
HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
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MIM; 601690; -.
InterPro; IPR000379; Est_lip_thioest_actsite.
InterPro; IPR000734; Lipase.
PROSITE; PS00120; LIPASE_SER; 1.
Hydrolase; Lipid degradation; Glycoprotein; Signal; Polymorphism;
                                                         Yamada Y., Ichihara S., Fulimura T., Yokota M.;
Yamada Y., Ichihara S., Fulimura T., Yokota M.;
"Identification of the G994--> T missense in exon 9 of the plasma platelet-activating factor acetylhydrolase gene as an independent risk factor for coronary artery disease in Japanese men.";
Metabolism 47:177-181(1998).
                                                                                                                                                                                                                                            VARIANT PHE-279.
MEDLINE-98430412; PubMed-9759612;
MEDLINE-98430412: PubMed-9759612;
Voshida H., Imaizuni T., Fujimoto K., Itaya H., Hiramoto M., ..
Yoshimizu N., Fukushi K., Satoh K.;
"A mutation in plasma platelet-activating factor acetylhydrolase (Val279Phe) is a genetic risk factor for cerebral hemorrhage but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
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I -> T (COMMON POLYMORPHISM;
DBSNP:1805018).
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CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
N-LINKED (GLCNAC. . .) (.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               asthma.";
Am. J. Hum. Genet. 66:1522-1530(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                   for hypertension.";
Thromb. Haemost. 80:372-375(1998).
VARIANT PHE-279.
MEDLINE-98132308; PubMed-9472966;
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FT VARIANT 279 279 V -> F (IN PLA2G7 DEFICIENCY; LOSS OF FUNCTION; MORE COMMON AMONE OF STATE TANN INSK FACTOR FOR CORONARY RET TO A CAUGASIANS; RISK FACTOR FOR CORONARY ARTHERY DISEASE AND STROKE).

FT YORIANT 281 281 0 -> R (IN PLA2G7 DEFICIENCY; LOSS OF FUT G-VAR_OLISS).

FT YORIANT 379 379 V -> A (COMMON POLYMORPHISM).

FT MUTAGEN 108 108 5->A: ACTIVITY:

MUTAGEN 278 286 D->A: ACTIVITY:

MUTAGEN 286 286 D->A: ACTIVITY:

FT MUTAGEN 286 286 D->A: ACTIVITY:

FT MUTAGEN 296 296 D->A: LOSS OF ACTIVITY:

FT MUTAGEN 304 304 D->A: LOSS OF ACTIVITY:

FT MUTAGEN 338 D->A: LOSS OF ACTIVITY:

FT MUTAGEN 338 338 D->A: LOSS OF ACTIVITY:

FT MUTAGEN 336 296 D->A: LOSS OF ACTIVITY:

FT MUTAGEN 336 296 D->A: LOSS OF ACTIVITY:

FT MUTAGEN 336 338 D->A: LOSS OF ACTIVITY:

FT MUTAGEN 338 338 D->A: LOSS OF ACTIVITY:

FT MUTAGEN 336 336 D->A: LOSS OF ACTIVITY:

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Search completed: July 1, 2002, 16:30:12 Job time: 621 sec

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Gaps

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Query Match 68.9%; Score 31; DB 1; Length 441; Best Local Similarity 71.4%; Pred. No. 77; Matches 5; Conservative 2; Mismatches 0; Indels

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097dnl clostridum
097dnl clostridum
04633 caenorhabdi
064597 arabidopsis
0459716 arabidopsis
029037 archaeoglob
089716 arabidopsis
045699 caenorhabdi
079080 lipolexis g
024pap human rotav
091h23 oryza sativ
091h23 oryza sativ
091h23 oryza sativ
099778 sus scrofa
09997 sus scrofa
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099718 sus scrofa
09997 are scrofa
099718 vus scrofa
09997 dictyostell
090836 dictyostell
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090843 dictyostell
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095416 aratus norv
091166 homo sapien
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Wilkinson J.;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequence of the nematode C.elegans: A platform investigating blology."; Science 282:2012-2018(198). EMBL; Z68099; 268041: -. SEQUENCE 858 AA; 96262 MW; 60E1070CA8F4D4C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
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                                     044623
064597
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Q9G7R8
Q9EML1
O94836
Q9VJN7
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Q98TR0
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Q9TDR1
O99997
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Q9NK83
Q9GRX5
Q9U987
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MEDLINE-99069613; PubMed-9851916;
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Q21853;
O1-NOV-1996 (TEMBLEEL 01, C.
01-NOV-1996 (TEMBLEEL 01, L.
01-DEC-2001 (TEMBLEEL 19, L.
R09A8.2 PROTEIN.
 88
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Best Local Similarity 75.0
Matches 6; Conservative
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Q21968 caenorhabdi
Q94417 bacillus ha
Q9x413 human immun
Q9zrf8 oryza sativ
Q9m625 hordeum vul
P93615 triticum ae
Q9cd90 mycobacteri
Q9cj05 lactococcus
Q9cj05 lactococcus
Q6cj12 equine rota
Q66772 equine rota
Q91687 human rotav
Q91687 human rotav
Q91687 aenopus lae
Q91687 aenopus lae
Q91687 aenopus lae
Q91687 aenopus lae
Q91687 arabidopsis
Q9fvs9 arabidopsis
                                                              July 1, 2002, 16:18:06; Search time 75.26 Seconds (without alignments) 18.389 Million cell updates/sec
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         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
                                               - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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sp_human:*
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115 AA.

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Chen L.J., Chai Y.J., Chen P.W.;
"A rice embryo-specific gene with high homology to soybean GmPM3 gene,
a hydrophoble LEA protein gene.";
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
EMBL: 057639; AAD10377.1; -.
SEQUENCE 173 AA; 18287 MW; 63FA2F778BB7259D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                           "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil."; Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; ARC79271.1; INTERPOOTOR: OF 20120.
Pfam: PF00516; GP120: 1.
Pfam: PF00516; GP120: 1.
MIDS: Coat protein; Glycoprotein.
                                                                                                                                                                                                                                                   Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A.,
Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       75.6%; Score 34; DB 15; Length 115; 62.5%; Pred. No. 31; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75.6%; Score 34; DB 10; Length 173;
85.7%; Pred. No. 46;
Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               12755 MW; 6551E67B32DCF56C CRC64;
                                                                                    01-WAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ENVELOPE GLYCOPROTEIN C2V3 REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYDROPHOBIC LEA-LIKE PROTEIN.
                                                                                                                                                             Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
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Best Local Similarity 62.5
Matches 5; Conservative
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                                                          PRELIMINARY;
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115 AA;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                        STRAIN=RJ96BRP071;
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78 NNTTFFFR 85
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NCBI_TaxID=4530;
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47 NGATFYF 53
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SEQUENCE
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                                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).
EMBL; AP001511; BAB04945.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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STRAIN=C-125 / JCM 9153;
MEDLINE-20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N., Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S., Horikoshi K.;
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                                                                                                                                                                                                                                                                                Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                          77.8%; Score 35; DB 5; Length 182; 75.0%; Pred. No. 31; Live 1; Mismatches 1; Indels
                                                                                                                                                                                          Coles i., Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                           investigating biology.";
Science 282:2012-2018 (1998).
EMBL: 250755; CASA0635.1;
InterPro: IPR001232; Skpl.;
Pfam: FF01466; Skpl; 1.
SEQUENCE 182 As, 21178 MW; 4BE38A19C4FA8124 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome.
SEQUENCE 71 AA; 8026 MW; 311AC9AEB3C539D3 CRC64;
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Last annotation update)
                                          Last sequence update)
Last annotation update)
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NCBI_TaxID=86665;
182 AA.
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                             Created)
PRT;
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                      01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-DEC-2001 (TrEMBLrel. 19,
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Best Local Similarity 75.0
در 6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
PRELIMINARY;
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                                                                                                  Caenorhabditis elegans.
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161 NNATLFFK 168
                                                                      R12H7.3 PROTEIN.
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173 AA

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Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K., Weissenbach J., Ehrlich S.D., Sorokin A.; "The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. lactis IL1403.", Genome Res. 11:731-753(2001).
EMBL; AE006258; AAK04299.1; -. HSSP; P39621; 1068.
                                                                                                                                                                                                         Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Squares S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Barrell B.G.;
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                                                                             Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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Pred. No. 71;
0; Mismatches 1; Indels
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273 AA; 30831 MW; D5B765A65EF39549 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-OCT-2001 (TrEMBLrel. 18, Last annotation update) HYPOTHETICAL PROTEIN ML0126.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
RHAMNOSYLTRANSFERASE.
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                                                                                                                                                                                                                                                                                                                                                                              "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  319 AA
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85.7%; Pred. No. 82;
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Pfam; PF00535; Glycos_transf_2; 1.
Transferase; Complete protecome.
SEQUENCE 319 AA; 37340 MW; DIDAC7
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85.7%;
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Best Local Similarity 85.77
Three 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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                                                                      Mycobacterium leprae.
                                                                                                                                                             SEQUENCE FROM N.A.
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20 NNAQFYF 26
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SEQUENCE 27
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"Accumulation of 19-kDa plasma membrane polypeptide during induction
of freezing tolerance in wheat suspension-cultured cells by abscisic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                       Hordeum vulgare (Barley).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticeae; Triticum.
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

Morris P.C., Ranford J.C.;

"Hordeum vulgare hydrophobic embryo-associated protein PM19 mRNA.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF218627; AAF29532.1; --
SEQUENCE 181 AA: 19036 MW; 849727F1123A4030 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Triticum aestivum (Wheat).
Eukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta;
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Pred. No. 48;
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?; 849727F1123A4030 CRC64;
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EMBL; U80037; AAB38504.1; -.
SEQUENCE 182 AA; 19009 MW; 799B9994AEA87DCB CRC64;
                                                                  01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
PLASMA MEMBRANE ASSOCIATED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1997 (TrEMBLrel. 03, Created)
U-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ABA INDUCED PLASMA MEMBRANE PROTEIN PM 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       273 AA.
                                  181 AA
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Pred. No.
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01-JUN-2001 (TrEMBLrel. 17, Created)
                                  PRT;
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MEDLINE-97393494; Pubmed-9249988;
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85.7%;
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ilarity 85.7%;
Conservative
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                                PRELIMINARY;
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Best Local Similarity
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Best Local Similarity
Matches 6; Conserv
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47 NGATEYE 53
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NGATFYF 53
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Griffin D.D., Nakagomi T., Hoshino Y., Nakagomi O., Kirkwood C.D., Griffin D.D., Alass R.I., Gentsch J.R.;
Parashar U.D., dlass R.I., Gentsch J.R.;
Parashar U.D., dlass R.I., Gentsch J.R.;
Parashar U.D., dlass R.I., Gentsch J.R.;
States:Identification of nontypeable rotavirus strains from the United States:Identification of a new rotavirus reassortant (P2A[6],G12) and rare P3[9] strains related to bowine rotaviruses.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ311738; CAC43312.1, 8897EDIDBBDIC981 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75.6%; Score 34; DB 12; Length 326; 62.5%; Pred. No. 84;
                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                          Viruses; dsRNA viruses; Reoviridae; Rotavirus.
NCBL_TaxID=10941;
                          326 AA.
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Xenopus laevis (African clawed frog).
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                            PRT;
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Best Local Similarity 85.7%;
Matches 6; Conservative (
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                                                                    01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, CAPSID PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 75.6
Best Local Similarity 62.5
Matches 5; Conservative
                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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318 NSATFYYR 325
                                                                                                                                                                                                          Human rotavirus.
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Q91655;
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  091E87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ciarlet M., Regget1 F., Pina C.I., Liprandi F.;
    "Equine rotaviruses with G14 serotype specificity circulate among
venezuelan horses.";
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Pred. No. 84; 0; Indels
3; Mismatches 0; Indels
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tive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00434; VP7; 1.
SEQUENCE 326 AA; 37296 MW; 9FC1BD4F4CC76529 CRC64;
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SEQUENCE 326 AA; 37352 MW; 9095E64B13933E29 CRC64;
                                                                                                                                                                      066771;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNOV-2001 (TrEMBLrel. 17, Last annotation update)
GLYCOPROTEIN VP7.
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Last annotation update)
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Viruses; dsRNA viruses; Reoviridae; Rotavirus.
NCBL_TaxID=10937;
                                                                                                                                                                                                                                                                                                                                 Viruses; dsRNA viruses; Reoviridae; Rotavirus NCBI_TaxID=10937;
                                                                                                                                                      326 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 venezuelan horses.";
J. Clin. Microbiol. 32:2609-2612(1994).
EMBL; UGS448; AAA81914.1;
Interpro; IPR001963; VP7.
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EMBL; U05349; AAA67342.1; -
InterPro; IPR001963; VP7.
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                                                                                                                                                      PRT;
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62.5%;
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01-NOV-1996 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. GLYCOPROTEIN VP7.
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Best Local Similarity
Matches 5; Conserv
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318 NSATFYYR 325
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|NSATFYYR 325
                                                                                                                                                                                                                                                                                                       Equine rotavirus.
1 NNATFYFK 8
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Brown D.D., Wang Z., Furlow J.D., Kanamori A., Schwartzman R.A.,
Remo B.F., Pinder A.;
"The thyroid hormone induced tail resorption program during Xenopus
                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                              lacvis metamorphosis.",
Proc. Natl. Acad. Sci. U.S.A. 93:1924-1929(1996).
EMBL; U41860; AAC59876.1; -.
Interpro; IPRO01507; zona_pellucida.
Pfam; PF00100; zona_pellucida; 1.
SMART; SM00241; ZP; 1.
SEQUENCE 357 AA; 39090 WW; 5493352C8EEA21E6 C
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A THOROIGS A., ECKET J.R., Palm C.J., Federspiel N.A., Kaul S.,

A THOROIGS A., ECKET J.R., Palm C.J., Federspiel N.A., Kaul S.,

A White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

A White D., Alonso J., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

RA Guldy M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dowar K.,

RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

RA Hutter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

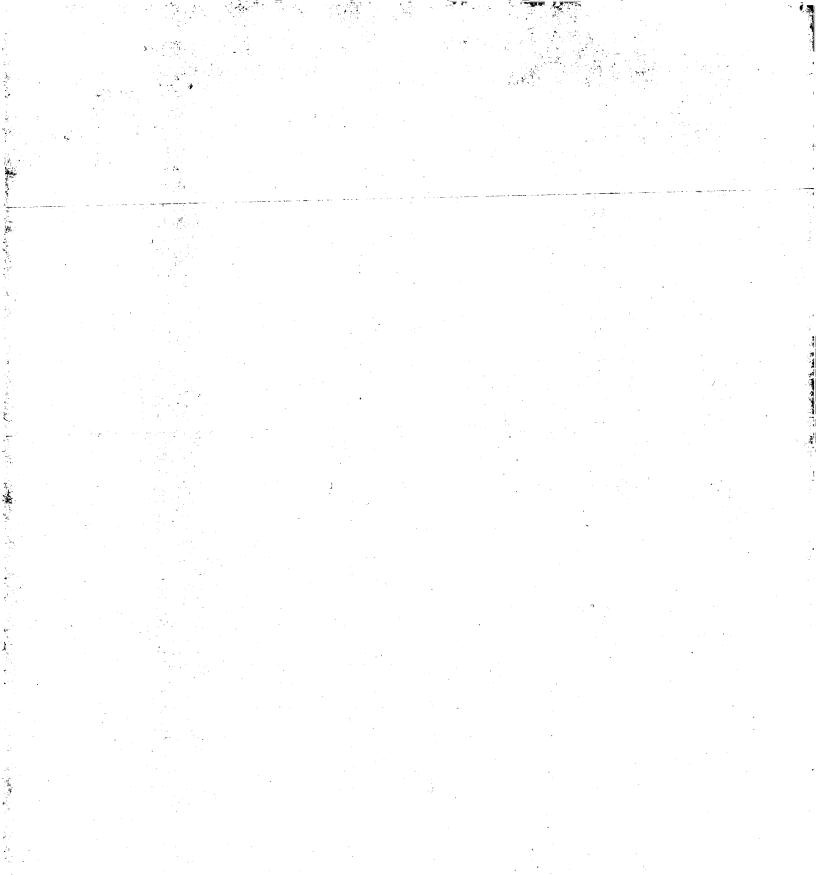
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

Militscher J., Miranda M., Nguyen M., Nlerman W.C., Osborne B.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                              Gray M.W.;
"The complete mitochondrial DNA sequences of Nephroselmis olivacea and Pedinomonas minor: two radically different evolutionary patterns within green algae.";
Plant Cell 11:1717-1729(1999).
                                                                                                                                                                                                    Mitochondrion.
Eukaryota; Viridiplantae; Chlorophyta; Pedinophyceae; Pedinomonadales;
Pedinomonadaceae; Pedinomonas.
NCBI_TaxID=3159;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Burger G.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
-1-CATALYIT CATIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
EMBL; AFIL6775; AD19671.1; -..
InterPro; IPR001750; Oxidored_q1.
Pfan; PF00361; Oxidored_q1.
Mitochondrion; NAD; Oxidored_q1.
SEQUENCE 440 AA; 51380 MW; C6D6CBAD72549B4C CRC64;
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                                            01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NADH DEHYDROGENASE SUBUNIT 2 (EC 1.6.5.3).
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1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01.5UN-2001 (TrEMBLrel. 17, Last annotation update)
CYTOCHAME P450, PUTATIVE.
  440 AA
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  PRT;
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SEQUENCE FROM N.A.
SEQUENCE LB 1350;
MEDLINE-99418884; Pubmed-10488238;
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PRELIMINARY;
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STRAIN-UTEX LB 1350;
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Best Local Similarity
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238 NNALFYF 244
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Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
An H., Tallon L.J., Tambunga G., Toriuni M.J., Town C.D.,
Utterback T., Van Aken S., Vaysberg M., Town C.D.,
W. Utterback T., Van Aken S., Vaysberg W.S., Walker M.,
"Sequence and analysis of chromosome 1 of the plant Arabidopsis
It haliana.";
In Nature 408:816-820(2000).
In Nature 408:816-820(2000).
In Richard M. Salzerg S. Cyt.P450.
R InterPro: IPR001128; Cyt.P450.
R InterPro: IPR001128; Cyt.P450.
R PRINTS; PR00385; P450.
R PRINTS; PR00385; P450.
R PRINTS; PR0086; CyTOCHROME_P450; UNKNOWN_1.
R PROSITE; PS0086; CyTOCHROME_P4506; WHOME SURVERSE.
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Pred. No. 1.3e+02;
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64 NLTFYFK 70
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Staphylococcus hom Escherichia coli p Bacillus sp. GUS p Bacillus sp. GUS p Bacillus sp. GUS p Staphylococcus bet Codon-optimised st Bacillus sp. GUS p Human immune/haema

Arabidopsis thalia Arabidopsis thalia

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Total number of

Database

Searched:

Perfect score:

Sequence:

OM protein

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Scoring table:

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Inhibition of mammalian legumain or legumain-related endopeptidase cystatin involves interaction with second papain-non-reactive site cystatin -
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AAM84819
AAG01238
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AAG44316
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AAG44314
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AAY81189
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AAB07996
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AAB37455
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RESULT
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Anti-angiogenic D3
Anti-angiogenic D3
Anti-angiogenic D3
Anti-angiogenic D3
Domaine 3, bradyki
Human kininogen D3
Human high mol.wt.
Novel human diagno
Novel human diagno

SIDSI/gogdata/hold-geneseq/geneseqp-embl/AAA1981.DMT:*
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SIDSI/gogdata/hold-geneseq/geneseqp-embl/AAA1981.DMT:*
SIDSI/gogdata/hold-geneseq/geneseqp-embl/AAA1981.DMT:*
SIDSI/gogdata/hold-geneseq/geneseqp-embl/AA1985.DMT:*
SIDSI/gogdata/hold-geneseqy-embl/AA1986.DMT:*
SIDSI/gogdata/hold-geneseqy-embl/AA1989.DMT:*
SIDSI/gogdata/hold-geneseqy-embl/AA1989.DMT:*
SIDSI/gogdata/hold-geneseqy-embl/AA1990.DMT:*
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SIDSI/gogdata/hold-geneseqy-embl/AA1992.DAT:*
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/SIDS1/gcgdata/hold-geneseq/genesegp-emb1/AA1981.
            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                hits satisfying chosen parameters:
                                                                                                                                                                                                                                       747574 seqs, 111073796 residues
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                                                              - protein search, using sw model
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AAY95410
AAY95408
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AAY95405
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Gapop 10.0 , Gapext 0.5
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The present invention relates to inhibition of the enzymatic activity of legumain or a legumain-related endopeptidase by cystatin. The inhibition involves an interaction between legumain and a papain-non-reactive site of cystatin. Legumain (EC 3.4.22.34) is a cysteine endopeptidase, and performs a protein-processing function. The present sequence is a peptide fragment of human kininogen D3, which was used in the present invention. Kininogen is a type 3 cystatin. The present sequence is thought to be involved in a legumain-inhibitory site.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence of AAY95406 or its N-terminal truncation fragment containing at least 1 amino acid"
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iive 0; Mismatches
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(MCCR/) MCCRAE R K.
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                            The present sequence is that of a D3 peptide derived from high mol.wt. kininogen (HK) domain 3 (see AAY95426). The D3 peptide, which may optionally include N-terminal and/or C-terminal protecting groups, inhibits endothelial cell proliferation and thus possesses anti-angiogenic activity. It is an example of peptides of the invention (see AAY95405-26) which are analogues of certain sites in the HK obmain 3, in this case amino acids Asn275-Lys282. The peptides inhibit endothelial cell proliferation and may also induce endothelial cell apoptosis. Compositions including such peptides are used in claimed methods for inhibiting anglogenesis, inhibiting endothelial cell proliferation, and inducing endothelial cell poptosis. Cancer, rheumatodia arthritis, and ocular disorders characterized by undesired vascularization of the retina are treated.
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100.0%; Pred. No. 0.051;
tive 0; Mismatches (
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Claim 1; Page 25; 44pp; English.
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Composition for inhibiting angiogenesis and endothelial cell proliferation, inducing endothelial cell apoptosis and treating cancer, rheumatoid arthritis, and ocular disorders comprises a kininogen domain
The peptides inhibit endothelial cell proliferation and may also induce endothelial cell apoptosis. Compositions including the peptides are used in claimed methods for inhibiting angiogenesis, inhibiting endothelial cell proliferation, and inducing endothelial cell proliferation, and inducing endothelial cell apoptosis. Cancer, rheumatoid arthritis, and ocular disorders characterized by undesired vascularization of the retina are treated. The ICSO value for the present peptide was less than 0.8 um for inhibition of fibroblast growth factor-induced HUVEC cell
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Composition for inhibiting angiogenesis and endothelial cell proliferation, inducing endothelial cell apoptosis and treating cancer, rheumatoid arthritis, and ocular disorders comprises a kininogen domain
                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is that of a D3 peptide derived from human high mol.wt. kininogen (HK) domain 3 (see AAV95426). The D3 peptide inhibits endothelial cell proliferation and thus possesses anti-anglogenic activity. It is an example of D3 peptides of the invention (see AAV95405-26) that are analogues of certain sites in the Case and Case and Case action sites in the peptides and cell proliferation and may also induce endothelial cell apoptosis. Compositions including the peptides in claimed methods for inhibiting anglogenesis, inhibiting endothelial cell proliferation, and inducing endothelial cell proliferation, and inducing endothelial cell apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            characterized by undesired vascularization of the retina are treated
                                                                                                                                                                                                                                                                                                                                                                                                      Anti-angiogenic; anglogenesis; inhibitor; kininogen; homologue; endothelial cell proliferation; apoptosis; cancer; ocular disorder; rheumatoid arthritis; cytotatic; antiarthritic; antirheumatic; therapy; human; D3 peptide.
The IC50 value for the present peptide was less than 0.8 uM for inhibition of fibroblast growth factor-induced HUVEC cell proliferation.
                                                                                                                                               ö
                                                                                                                 100.0%; Score 45; DB 21; Length 16; 100.0%; Pred. No. 0.082;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 21; Length 32;
                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 45; DB 2. Pred. No. 0.17;
                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                AAY95408 standard; Peptide; 32 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Page 26; 44pp; English.
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100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US28465.
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                                                                                                                                                                                                                                                                                                                                                                        Anti-angiogenic D3 peptide.
                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                               Conservative
                                                                                              Query Match
Best Local Similarity
8; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UTEM ) UNIV TEMPLE. (MCCR/) MCCRAE R K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-442247/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                      16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32 AA
                                                                                                                                                                                            1 NNATFYFK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200035407-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-DEC-1999;
                                                                                                                                                                                                                                                                                                                                             25-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-JUN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  McCrae RK;
                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sednence
                                                                                                                                                                                                                                                                                                              AAY95408;
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Mismatches

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-Matches

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AAR33350 RESULT

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The present invention relates to inhibition of the enzymatic activity of legumain or a legumain related endopeptidase by cystatin. The inhibition involves an interaction between legumain and a papain-non-reactive site of cystatin. Legumain (EC 3.4.23.44) is a cysteine endopeptidase, and performs a protein-processing function. The present sequence is human kininogen D3, which was used in the present invention. Kininogen is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inhibition of mammalian legumain or legumain-related endopeptidase by cystatin involves interaction with second papain-non-reactive site of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anti-angiogenic; angiogenesis; inhibitor; kininogen; homologue; endofibelial cell proliferation; apoptosis; cancer; ocular disorder; rheumatoid arthritis; cytostatic; antiarthritic; antirheumatic; therapy; human; D3 peptide.
                                                                                                                                                                                                                          Enzyme; legumain; endopeptidase; cystatin; human; kininogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 45; DB 21; ilarity 100.0%; Pred. No. 0.67; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human high mol.wt. kininogen domain 3.
                                                             AAB37447 standard; protein; 122 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; Peptide; 123 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 4; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                         20-APR-2000; 2000WO-GB01571.
                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barrett AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BABR-) BABRAHAM INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-687316/67.
                                                                                                                                                                                    Human kininogen D3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      type 3 cystatin.
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                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                 22-APR-1999;
                                                                                                                                              21-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                 02-NOV-2000
                                                                                                     AAB37447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY95426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cystatin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY95426
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                                                                                    셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence given represents domain 3, amino acids 246-362, of the human kininogen heavy chain. Domain 3 was isolated from low molecular weight kininogen, derived from human plasma. by cleavage with trypsin. Domain 3 peptide inhibits platelet activation causing a marked decrease in the platelets ability to aggregate and secrete their granule contents. The granule contents comprise proteins which participate in hemostasis, thrombosis and the inflammatory response. Domain 3 also inhibits endothelial cell activation shown by a decrease in secretion of endothelial cell contents such as tissue plasminogen activator and won Willebrand factor. Domain 3 functions to inhibit cell activation by blocking thrombin binding to its target cells, the peptide is a selective inhibitor of thrombin-induced platlet.
                                                                                                                                                                                                                                                                                                    Domain 3; human; kininogen; heavy chain; low molecular weight; plasma; trypsin; platelet; activation; granule contents; hemostasis; thrombin; tissue plasminogen activator; thrombosis; inflammatory response; endothelial cell; von Willebrand factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of trypsin-cleavage fragment of human kininogen - for increasing vascular bradykinin release, for lowering blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                              Domaine 3, bradykinin release activating peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Leader peptide"
19.117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                       AAR33350 standard; protein; 117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pressure and treating hypertension
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 1; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92WO-US06809
                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jiang Y, Schmaier AB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UTEM ) UNIV TEMPLE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 AA;
                         NNATEYEK 8
NNATFYFK 8
                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-AUG-1992;
                                                                                                                                                                                                                        01-JUL-1993
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WO9303748-A. 04-MAR-1993

Peptide Protein ö

Gaps

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0; Indels

Homo sapiens

activation.

Sequence

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Length 122;

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO. At the wipo.int, pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                       New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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100.0%; Score 45; DB 22; Length 248;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 8; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                       Claim 20; SEQ ID No 51461; 103pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG21099 standard; Protein; 369 AA.
                    Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0540217.
2000US-0649167.
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                                                             WPI; 2001-639362/73.
N-PSDB; AAS85289.
                    Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC
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90 nnatfyfk 97
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                    Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-OCT-2001.
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                                                                                                                                                                                                                                                                                                                                          Composition for inhibiting angiogenesis and endothelial cell proliferation, inducing endothelial cell apoptosis and treating cancer, rheumatoid arthritis, and ocular disorders comprises a kininogen domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is that of domain 3 of human high mol.wt. kininogen (HK). The invention provides peptides (see AAY95405-24) that are analogues of certain sites in the HK domain 3, specifically Asn275-Lys282, Cys246-Cys249, Leu331-Tyr338 and Tyr299-Ser314. The peptides, in which native Cys residues may be replaced by A har residues, inhibit endothelial cell proliferation and may also induce endothelial cell apoptosis. Compositions including the peptides are used in claimed methods for inhibiting angiogenesis, inhibiting endothelial cell proliferation, and inducing endothelial cell apoptosis. Cancer, rheumatoid arthritis, and ocular disorders characterized by undesired vascularization of the retina are treated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 4; 44pp; English.
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Matches 8; Conservative
                                                                                                                                                                                       (UTEM ) UNIV TEMPLE. (MCCR/) MCCRAE R K.
                                                                                                                                                                                                                                                                                                   WPI; 2000-442247/38.
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                  WO200035407-A2.
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                                                                                                     02-DEC-1999;
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                                                                                                                                                16-DEC-1998;
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                                                           22-JUN-2000
                                                                                                                                                                                                                                                            McCrae RK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG21102;
                                                                                                                                                                                                                                                                                                                                                                                                                 3 analog
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PRR) primers, oligomer, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to tread disease states involving quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human and amino acid sequences of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                            New isolated polynucleotide and encoded polypeptides, useful in haldgrostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 45; DB 22; Length 369; 100.0%; Pred. No. 2.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                         Claim 20; SEQ ID No 51458; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human diagnostic protein #21092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG21101 standard; Protein; 644 AA.
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 Tang YT;
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 8; Conservative
                      WPI; 2001-639362/73.
Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drmana& RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                   369 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          333 nnatfyfk 340
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                                    N-PSDB; AAS85286
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The invention relates to isolated polynucleotide (I) and probes, colympeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The colynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving to restore normal activity of (II) or to treat disease states involving a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and canno acid sequences. ABGO0010-ABG30377 represent novel human DNA and diagnostic amino acid sequences of the invention.

Specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                     Claim 20; SEQ ID No 51460; 103pp; English.
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Best Local Similarity 100.

Matches 8; Conservative
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WPI; 2001-639362/73.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           293 nnatfyfk 300
                                     N-PSDB; AAS85288
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                                                                                                                                                                                                               biodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; cytokine; cell proliferation; cell differentiation; gene therapy; vacchie; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                Administration of a peptide or multimer related to bradykinin or other disclosed peptides and multimers can be used for the inhibition of thrombin-induced platelets or other cells. They can also be used for preventing platelet aggregation, or inhibiting ADP-induced activation. This is useful to prevent arterial occlusions arising from coronary thrombosis and stroke.
                                                                                                                                                                                                                                                                                                        Gaps
              Inhibition of platelet activation and aggregation - by admin. of new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune disorders -
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                                                                                                                                                                                                                                                                       DB 18; Length 26;
1.6;
                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                              86.7%; Score ...
100.0%; Pred. No. 1.6;
-+iva 0; Mismatches
                                                                 Disclosure; Page 44; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human polypeptide SEQ ID NO 18972.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA005080 standard; Protein; 78 AA.
                                   known bradykinin analogues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang YT, Liu C, Drmanac RT
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18-MAY-2000; 2000US-0577409
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                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.00
Best Accal 7; Conservative
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                                                                                                                                                                                                                       26 AA;
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|natfyfk 7
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                                                                                                                                                                                                                                                                                                                                        NATFYFK 8
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                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer associated nucleic and molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vacchee production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally. N may be used to produce the colon cancer associated Ps, by inserting the nucleic acids into a host cell and culturing the cell or express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the
                                 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
treatment of cancer, leukaemia, nervous system disorders, arthritis and
inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers - \,
                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               colon cancer; colon cancer antigen; diagnosis; detection;
                                                                                                                                                                                           ö
                                                                                                                                                        Length 78;
                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human colon cancer antigen protein SEQ ID NO:5142.
                                                                                                                                                        22;
                                                                                                                                                        Score 36; DB 2
Pred. No. 18;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                      AAG74378 standard; Protein; 42 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Birse CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                          80.0%;
85.7%;
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99US-0163280.
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                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                        Query Match 80.0
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    colorectal carcinoma
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                                                                                                          AA;
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                                                                                                                                                                                                                                                          38 nnttfyf 44
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                                                                                                        78
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03-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                        AAG74378;
                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human;
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                                                                                                                                                                                                                                                                                                                    RESULT
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The present sequence is a microbial beta-glucuronidase (GUS)

protein. GUS genes were obtained from six different genera:

Enterobacter/Salmonella, pseudomonas, Salmonella, Staphylococcus and
Thermotoga. Microbial GUS can be used as a reporter/effector molecule for
transgenic constructions and in in vitro diagnostic applications. It may
also be used to generate sentinel plants that serve as bioindicators of
environmental status. It may be used to generate transgenic insects for
bioassay for compounds that affect molecules critical for insect
development (e.g. juvenile hormone). Secreted GUS may also serve as a
marker for beneficial fungi destined for release into the environment.

Comparains, secreted GUS may be used to achieve extracellular
animal systems, secreted GUS may be used to achieve extracellular
conjugation patterns of glucuronides. Microbial GUS may also be used in
traditional medical adiagnostic assays, for drug testing, pharmacokinetic
studies, bloavallability studies, diagnosis of diseases and syndromes,
following progression of disease or its response to therapy. Microbial
activity. It is highly specific for the substrate and water soluble, and
the substrates are stable.
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                                                                                                                                                                                                                                                                                                                                                                                                 Microbial; beta-glucoronidase; GUS; Enterobacter; Salmonella; Pseudomonas; Staphylococcus; Thermotoga; transgenic plant; bioindicator; transgenic insect; marker; glucuronide detoxification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel microbial beta-glucuronidase genes and gene products used as reporter/effector molecule, as diagnostic tool, in positive selection, to target molecules to specific cells and to detect and track linked
                                                                                                     Gaps
                                                                                                   0;
                                                           Score 34; DB 22; Length 42;
Pred. No. 21;
                                                                                                   1; Indels
                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus homini beta-D-glucoronidase
                                                                                                                                                                                                                                                            AAB28404 standard; Protein; 376 AA.
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                                                            75.6%;
85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-MAR-2000; 2000WO-US07107
                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                     6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jefferson RA, Mayer JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus homini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-647075/62.
                                                            Query Match
Best Local Similarity
              42 AA;
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                                                                                                                                                                       22 nratfyf 28
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                                                                                                                                    1 NNATFYF 7
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                                                                                                                                                                                                                                                                                                                                26-JAN-2001
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MEDLINE=85122621; PubMed=6441591;
Ohkubo I., Kurachi K., Takasawa T., Shiokawa H., Sasaki M.;
Ohkubo I., Rurachi K., Takasawa T., Shiokawa H., Sasaki M.;
Isolation of a human cDNA for alpha 2-thiol proteinase inhibitor and its identity with low molecular weight kininogen.";
Biochemistry 23:5691-5697(1984).
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"Structural organization of the human kininogen gene and a model for
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MEDLINE=86030270; PubMed-4054110;
Lottspeich F., Kellermann J., Henschen A., Foertsch B.,
Mueller-Esterl W.;
"The amino acid sequence of the light chain of human high-molecularmass kininogen.";
                                                                                                                                                                                                                                                                               KNG_HUMAN STANDARD; PRT; 644 AA.
P01042; P01043;
21-JUL-1986 (Rel. 31. Last sequence update)
16-OCT-2001 (Rel. 40. Last annotation update)
16-OCT-2001 (Rel. 40. Last annotation update)
Bradykinin].
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BADLINE-B6234582; PubMed=2989293;

Takegaki Y., Kitamura N., Nakanishi S.;

"Cloning and sequence analysis of cDNAs for human high molecular weight and low molecular weight and low molecular weight prekininogens. Primary structures two human prekininogens.";

J. Biol. Chem. 260:8601-8609(1985).
                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
bisArzyota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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P40175 :
Q27727 |
P17544 |
Q99257 :
P46000 :
Q13255 |
P23385 :
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"Disulfide bonds in bovine HMW kininogens.";
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                                                                                                                                                                                                             ALIGNMENTS
                NUSG_MYCTU
CYSH_SYNY3
FFU2_BACST
FFT3_STRRA
EFT3_STRCO
ENO_PLAFA
ATF7_HUMAN
MX67_YEAST
FASD_ECOLI
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PSK5_ARATH
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"Structural features of plasma kinins
Fed. Proc. 27:52-57(1968).
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MEDLINE-85234583; PubMed-2989294;
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Copyright (c) 1993 - 2000 Compugen Ltd.
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HMW-KININGGEN PLAYS AN IMPORTANT ROLE IN BLOOD COAGULATION BY
HELPING TO POSITION OPTIMALLY PREKALLIKREIN AND FACTOR XI NEXT TO
FACTOR XIL; (3) HMW-KININGEN INHIBITS THE THROMEIN-AND PLASMIN-
INDUCED AGGREGATION OF THROMBOCYTES; (4) THE ACTIVE PEPTIDE
BRADYKININ THAT IS RELEASED FROM HWW-KININGEN SHOWS A VARIETY OF
PHYSIOLOGICAL EFFECTS: (4A) INFLUENCE IN SMOOTH MUSCLE
CONTRACTION, (4B) INDUCTION OF HYPOTENSION, (4C) NATRICRESIS AND
DIURESIS, (4D) DECREASE IN BLOOD GLUCOSE LEVEL, (4E) IT IS A
MEDIATOR OF INFLAMMATION AND CAUSES (4E1) INFREASE IN VASCULAR
PERMEABILITY, (4E2) STIMULIATION OF NOCICEPTORS (4E3) RELEASE OF
OTHER MEDIATORS OF INFLAMMATION (E.G. PROSTAGLANDINS), (4F) IT HAS
A CARDIOPROTECTIVE EFFECT (DIRECTLY VIA BRADYKININ ACTION,
INDIRECTLY VIA ENDOTHELIUM-DERIVED RELAXING FACTOR ACTION); (5)
LWW-KININGEN INHIBITS THE AGSREGATION OF THROMBOCYTES; (6) LAW-
KININGEN IS IN CONTRAST TO HMW-KININGEN NOT INVOLVED IN BLOOD
                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00287; CYSTATIN; 2. Glycoprotein; Plasma: Repeat; Thiol protease inhibitor; Vasodilator; Bradykinin; Blood coagulation; Inflammatory response; Signal; Alternative splicing. 1 18
                                                                                                                                                                                                                      ALTERNATIVE PRODUCTS: 2 ISOFORMS; HWW (SHOWN HERE) AND LAW; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: PLASMA.
                                                                                                                                                                                                                                                       PTM: BRADYKININ IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN. SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
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InterPro; IPR000010; Cystatin.
InterPro; IPR003243; Cystatin.C.M.
InterPro; IPR00235; Kininogen.
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PRINTS; PR00334; KININOGEN.
PLODOM; PD001231; Cystatin_C_M; 1.
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PIR; B25276, B25276.
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Seikagaku 56:808-808(1984)
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Nawa H., Kitamura N., Hirose T., Asai M., Inayama S., Nakanishi S.;
"Primary structures of bovine liver low molecular weight kininogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Kininogen, LMW I precursor (Thiol proteinase inhibitor) [Contains: Bradykinin].
Bos taurus (Bovine).
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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Proc. Natl. Acad. Sci. U.S.A. 80:90-94(1983).
[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                              INTERCHAIN.
KININOGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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Best Local Similarity 100.
Matches 12; Conservative
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NCBI_TaxID=9913;
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593
644 AA;
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                                                                                                                                            KNL1_BOVIN
P01046;
                                                                                                                                                                                               MOD_RES
DISULFID
                                                                                                                                                                                                                                                                             DISULFID
DISULFID
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CARBOHYD
VARSPLIC
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                              PEPTIDE
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Gaps

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Indels

1;

2; Mismatches

Conservative

8

Matches

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                                           Miyata T., Iwanaga S.;

Bovine high molecular weight kininogen. The amino acid sequence,

Bovine high molecular weight kininogen. The amino acid sequence,

The chain portion.

J. Blol. Chem. 262:2768-2779(1987)

I. Blol. Chem. 262:2768-2779(1987)

I. Blol. Chem. 262:2768-2779(1987)

I. Blol. Chem. 262:2768-2779(1987)

I. MA-KININOGEN INHIBITS THE AGREGATION OF THROMBOCYTES; (2)

I.W.-KININOGEN INHIBITS THE AGREGATION OF THROMBOCYTES; (3) THE

A VARIETY OF PHYSICIOGICAL EPPECTS: (3A) INFLUENCE IN SMOTH

MUSCLE CONTRACTION, (3B) INDUCTION OF HYPOTENSION, (3C)

NATRIURESIS AND DIURESIS (KIDNEY).

SUBCELLULAR LOCATION: Extracellular.

-I- ALTERNATIVE PRODUCTS: HWM I AND LMM I KININOGEN PRECURSORS ARE

PRODUCED FROM THE SAME GENE AS THE RESULT OF ALTERNATE MRNA

SPLICING: THE SEQUENCES OF BOTH KININOGENS ARE IDENTICAL UP
                                                                                                                                                                                                                                                                                  TO RESIDUE 400.
-!- TISSUE SPECIFICITY: PLASMA.
-!- PTM: BRADYKININ IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN.
-!- MISCELLANEOUS: LMW-KININOGEN IS IN CONTRAST TO HMW-KININOGEN NOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00287; CYSTATIN; 2.
Glycoprotein; Plasma; Repeat; Vasodilator; Alternative splicing;
Thiol protease inhibitor; Bradykinin; Signal.
SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYSTATIN-LIKE 1.
CYSTATIN-LIKE 2.
CYSTATIN-LIKE 2.
CYSTATIN-LIKE 2.
PYRROLIDONE CARBOXYLIC ACID.
N-LINKED (GLCNAC. . .).
O-LINKED (GLCNAC. . .); OR 169.
N-LINKED (GLCNAC. . .); OR 169.
N-LINKED (GLCNAC. . .) (PARTIAL).
N-LINKED (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PARTIAL)
                MEDLINE-87137530; PubMed-3546295;
Sueyoshi T., Miyata T., Hashimoto N., Kato H., Hayashida H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -> T (IN REF. 1; CAA23709).
F01F7EB6814BCE6C CRC64;
                                                                                                                                                                                                                                                                                                                                              INVOLVED IN BLOOD CLOTTING.
-1- SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KININOGEN, LMW I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HEAVY CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BRADYKININ.
LIGHT CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERCHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A01283; KGBOL1.
InterPro; IPR000010; Cystatin.
InterPro; IPR003243; Cystatin_C_M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Cystatin_C_M; 1. CY; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48427 MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; V00426; CAA23709.1; -. EMBL; J00010; AAA30604.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00031; cystatin; 3
ProDom; PD001231; Cystatin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    327
350
295
436 AA;
 SEQUENCE OF 19-378.
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168
197
204
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Length 436;

Score 42; DB 1; Pred. No. 1.4;

70.0%; 72.7%;

Query Match Best Local Similarity

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MEDLINE-7510265; Pubmed-1169237;
Anny Y.N., Komiya M., Iwanaga S., Suzuki T.;
Han Y.N., Komiya M., Iwanaga S., Suzuki T.;
Kininogen. Amino a caid sequence of a fragment ('histidine-rich peptide') released by plasma kallikrein.";
L. J. Biochem. 77:55-68(1975).
L. J. Biochem. 77:55-68(1975).
C. I. FUNCTION: (1) KININOGENS ARE INHIBITORS OF THIOL PROTEASES; (2)
HWW-KININOGEN PLAYS AN IMPORTANY ROLE IN BLOOD COAGULATION BY HELPING TO POSITION OPTIMALLY PREKALLIKREIN AND PACTOR XII.; (3) HWW-KININOGEN KII. (4) THE ACTIVE PEPTIDE BRADYKININ THAT IS RELEASED FROM HWW-KININOGEN SHOWS
C. PREPTIDE BRADYKININ THAT IS RELEASED FROM HWW-KININOGEN SHOWS
C. A VARIETY OF PHYSIOLOGICAL EFFECTS: (4A) INFLUENCE IN SMOOTH
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDIJUBE-84014106; PubMed-6571699; MEDIJUBE-84014106; PubMed-6571699; Kitamura N., Takagaki Y., Furuto S., Tanaka T., Nawa H., Nakanishi S.; "A single gene for bovine high molecular weight and low molecular."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=70180420; PubMed=4986212; Kato H., Nagasawa S., Suzuki T.; Kato H., Nagasawa S., Suzuki T.; Studies on the structure of bovine kininogen: cleavages of disulfide bonds and of methionyl bonds in kininogen-II."; J. Biochem. 67:313-323(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 19-378.
MEDLINE=87137530; PubMed=3546295;
Sueyoshi T., Miyata T., Hashimoto N., Kato H., Hayashida H.,
Miyata T., Iwanaga S.;
"Bovine high molecular weight kininogen. The amino acid sequence,
positions of carbohydrate chains and disulfide bridges in the heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MUSCILE CONTRACTION, (4B) INDUCTION OF HYPOTENSION, (4C)
NATRUDESIS AND DIURESIS, (4D) DECRRASE IN BLOOD GLUCOSE LEVEL,
(4E) IT IS A MEDIATOR INFLAMMATION AND CAUSES (4E1) INCREASE
IN VASCULAR PERMEABLILIY, (4E2) STIMULATION OF NOCICEPTORS (4E3)
RELEASE OF OTHER MEDIATORS OF INFLAMMATION (E.G. PROSTAGLANDINS)
(4F) IT HAS A CARDIOPROTECTIVE EFFECT (DIRECTLY VIA BRADYKININ
ACTION, INDIRECTLY VIA ENDOTHELLUM-DERIVED RELAXING FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Extracellular.
ALTERNATIVE PRODUCTS: HMW I AND LMW I KININOGEN PRECURSORS ARE
PRODUCED FROM THE SAME GENE AS THE RESULT OF ALTERNATE MRNA
SPLICING: THE SEQUENCES OF BOTH KININOGENS ARE IDENTICAL UP
TO RESIDUE 400.
                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-MMR-2002 (Rel. 41, Last annotation update)
Kininogen, HWW I precursor (Thiol proteinase Inhibitor) (Contains: Bradykinin).
                                                                                                                                                                                                                                                                                                Bos ťaurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
                                                                                                                                               621 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chain portion.";
J. Biol. Chem. 262:2768-2779(1987).
                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE SPECIFICITY: PLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 305:545-549(1983).
                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                  Bovidae; Bovinae; Bos.
                         |:|:| |||||
281 LSHSIAKLNAE 291
2 LTHTITKLNAE 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 378-393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        kininogens
                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9913;
                                                                                        KNH1_BOVIN
ID KNH1_BOVIN
AC P01044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      weight
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us-09-461-061a-2.open.rsp

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NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                    chain portion.";
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DOMAIN
MOD_RES
CARBOHYD
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DISULFID
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CHAIN
PEPTIDE
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                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PTM: BRADYKININ IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
11-JUL-1986 (Rel. 41, Last annotation)
11-JUL-1986 (Rel. 41, Last sequence update)
11-JUL-1986 (
                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002395; Kininogen.
PRINTS; PR0031; cystatin; 3.
PRINTS; PR0031; cystatin; 3.
PRODOM; PR001221; Cystatin_C_M; 1.
SWART; SW00043; CY; 3.
PROSITE; PS00287; CYSTATIN; 2.
ROSCITE; PS00287; CYSTATIN; 2.
ROSCITE; PS00287; CYSTATIN; 2.
RIJOA protease inhibitor; Bradykinin; Blood coagulation;
Inflammatory response; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PYRROLIDONE CARBOXYLIC ACID.
N-LINKED (GLCNAC. . .).
O-LINKED (FARTIAL).
N-LINKED (GLCNAC. . .); OR 169.
N-LINKED (GLCNAC. . .) (PARTIAL).
N-LINKED (GLCNAC. . .).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68890 MW; D16850BEFE3C55CD CRC64;
                           !- SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KININOGEN, HWW I.
HEAVY CHAIN.
BRADYKININ.
LIGHT CHAIN.
CYSTATIN-LIKE 1.
CYSTATIN-LIKE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           434 AA.
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2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROBABLE.
                                                                                                                                                                                                                                                                                                                                 Interpro; IPR000010; Cystatin.
Interpro; IPR003243; Cystatin_C_M.
Interpro; IPR002395; Kininogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                     EMBL; V01491; CAA24735.1; -.
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Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                              PIR; A01281; KGBOH1.
PIR; A29559; A29559.
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281 LSHSIAKLNAE 291
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P01047;
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MOD_RES
CARBOHYD
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JULIO CHANGE SERVICE STATEMENT OF THIOL PROTEASES; (2)

1. FUNCTION: (1) KININOGENS ARE INHIBITORS OF THIOL PROTEASES; (2)

1. FUNCTION: (1) KININOGENS ARE INHIBITORS OF THIOL PROTEASES; (2)

1. FUNCTION: (1) KININOGENS ARE INHIBITORS OF THOOLBOCYTES; (3) THE

ACTIVE PEPTIDE KALLIDIN THAT IS RELEASED FROM LAW-KININOGEN SHOWS

A VARIETY OF PHYSIOLOGICAL EFFECTS: (3A) INFLUBNCE IN SMOOTH

MUSCLE CONTRACTION, (3B) INDUCTION OF HYPOTENSION, (3C)

NATHIURESIS AND DIURESIS (KINDEY).

1. SUBCELLOLAR LOCATION: Extracellular.

1. ALTERNATIVE PRODUCTS: HWW II AND LAW II KININOGEN PRECURSORS ARE

PRODUCED FROM THE SAME GENE AS THE RESULT OF ALTERNATE MRNA

SPLICING. THE SEQUENCES OF BOTH KININOGENS ARE IDENTICAL UP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- TISSEE SPECIFICITY: PLASMA.
-1- PTM: BRADYKININ IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN.
-1- MISCELLANEOUS: LMM-KININOGEN IS IN CONTRAST TO HMW-KININOGEN NOT
                                    MEDIINE-83117859; PubMed-6572010;
Nawa H., Kitamura N., Hirose T., Asai M., Inayama S., Nakanishi S.;
"Primary structures of bovine liver low molecular weight kininogen
                                                                                                                                                                                                                                                                                                                                                                                          Miyata T., Iwanaga S.;
"Bovine high molecular weight kininogen. The amino acid sequence,
positions of carbohydrate chains and disulfide bridges in the heavy
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Glycoprotein; Plasma; Repeat; Vasodilator; Alternative splicing;
Thiol protease inhibitor; Bradykinin; Signal.
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CYSTATIN-LIKE 1.

CYSTATIN-LIKE 2.

CYSTATIN-LIKE 2.

CYSTATIN-LIKE 2.

CYSTATIN-LIKE 3.

PYRROLIDONE CARBOXYLIC ACID.

N-LINKED (PARTIAL).

N-LINKED (GLCNAC. . .); OR 169.

N-LINKED (GLCNAC. . .) (PARTIAL).

N-LINKED (GLCNAC. . .)

N-LINKED (GLCNAC. . .)
                                                                                                                                                                                                                                     [2]
SEQUENCE OF 19-376.
MEDLINE=87137530; PubMed=3546295;
Sueyoshi T., Miyata T., Hashimoto N., Kato H., Hayashida H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INVOLVED IN BLOOD CLOTTING.
-1- SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KININOGEN, LAW II.
                                                                                                                                                            precursors and their two mRNAs.";
Proc. Natl. Acad. Sci. U.S.A. 80:90-94(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HEAVY CHAIN.
BRADYKININ.
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InterPro; IPR000010; Cystatin.
InterPro; IPR003243; Cystatin.C_M.
Pfam; PF00031; cystatin; 3.
Probom; PD0001231; Cystatin_C_M; 1.
SWART; SM00043; CY; 3.
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SEQUENCE FROM N.A.
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PIR; S05381; S05381
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                                          SIGNAL
                                                                    DOMAIN
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KNH2_BOVIN
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            ET ET SO
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                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=91203852; PubMed=2017159;
Salton S.R.J., Fischberg D.J., Dong K.-W.;
"Structure of the gene encoding VGF, a nervous system-specific mRNA that is rapidly and selectively induced by nerve growth factor in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-92309005; PubMed=1377233; Hawley R.J., Scheibe R.J., Wagner J.A.; "NGF induces the expression of the VGF gene through a cAMP response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Neurosci. 12:2573-2581(1992).
-I- FUNCTION: MAY BE INVOLVED IN THE REGULATION OF CELL-CELL INTERACTIONS OR IN SYNATOGENESIS DURING THE MATURATION OF THE
                                                                                                                                          ;
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MEDLINE=90005425; PubMed=2676516;
MEDLINE=90005425; PubMed=2676516;
Possentl R., Eldridge J.D., Paterson B.M., Grasso A., Levi A.;
RA protein induced by NGF in PC12 cells is stored in secretory vesicles and released through the regulated pathway.";
EMBO J. 8:2217-2223(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NERVOUS SYSTEM.
--- SUBCELLIDIAR LOCATION: SECRETORY VESICLES.
--- TISSUE SPECIFICITY: CENTRAL AND PERIPHERAL NERVOUS TISSUE.
--- INDUCTION: BY NGF.
                                                                                                             Length 434;
                                                                                                                                         2; Indels
                                                                   48148 MW; 73A7079DE3E03430 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (OCT-1995) to the SWISS-PROT data bank.
                                                                                                             Score 41; DB 1;
                                                                                                                                                                                                                                                                                                   01-FEB-1991 (Rel. 17, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
12-JUL-1998 (Rel. 36, Last annotation update)
VGF protein precursor (VGF8A protein).
                                                                                                                           Pred. No. 2.1;
                                                                                                                                                                                                                                                                         617 AA
                                                                                                                                         1; Mismatches
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                                                                                                            68.3%;
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EMBL; M60525; AAA86428.1; -.
EMBL; M74223; AAA42336.1; -.
                                                                                                                                         Conservative
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279 LNHSIAKLNAE 289
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       228
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325
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434 AA;
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P20156;
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Kato H., Nagasawa S., Suzuki T.;
"Studies on the structure of bovine kininogen: cleavages of disulfide
bonds and of methionyl bonds in kininogen-II.";
J. Biochem. 67:313-323(1970).
                                                                                                                                                                                                                                                                                                                      Gaps
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MEDILINE-76560155; PubMed-956151;
MEDILINE-76560155; PubMed-956151;
Han Y.N., Kato H., Iwanaga S., Suzuki T.;
"Primary structure of bovine plasma high-molecular-weight kininogen."
The amino acid sequence of a glycopeptide portion (fragment 1)
following the C-terminus ot the bradykinin moiety.";
J. Biochem. 79:1201-1222(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 41, Last annotation update)
Kininogen, HAW II precursor (Thiol proteinase inhibitor) [Contains: Bradykinin].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-87137530; PubMed-3546295; Sueyoshi T., Miyata T., Hashimoto N., Kato H., Hayashida H., Miyata T., Iwanaga S.; Miyata T., Iwanaga S.; Bovine high molecular weight kininogen. The amino acid sequence, positions of carbohydrate chains and disulfide bridges in the heavy
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MEDLINE-75.710265; PubMed=1169237;

Han Y.N., Komiya M., Iwanaga S., Suzuki T.;

Han Y.N., Komiya M., Iwanaga S., Suzuki T.;

Studies on the primary structure of bovine high-molecular-weight kininogen. Amino acid sequence of a fragment ('histidine-rich peptide') reteased by plasma kallikrein.";

peptide') reteased by plasma kallikrein.";

J. Blochem. 77:55-68(1975).

-: FUNCTION: (1) KININOGENS ARE INHIBITORS OF THIOL PROTEASES; (2) HMW-KININOGEN PLAYS AN IMPORTANT ROLE IN BLOOD COAGULATION BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-84014106; PubMed-6571699; Kitamura N., Takagaki Y., Furuto S., Tanaka T., Nawa H., Nakanishi "A single gene for bovine high molecular weight and low molecular weight kininogens.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus (Bovine).
Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos
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                                                                                                                                                                                                                                                       Length 617;
                                                                                                                                                                                                                                                                                                                   2; Indels
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A41A447CD51F67B6 CRC64;
                                                        VGF PROTEIN.
ASP/GLU-RICH (ACIDIC).
                                                                                                                                                                                                                                                Score 41; DB 1;
Pred. No. 3.1;
3; Mismatches
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                                    POTENTIAL.
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                                                                                                                                                         68192 MW;
                                                                                                                                                                                                                                                       68.3%;
58.3%;
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Best Local Similarity 58.30,
7; Conservative
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617
452
342
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190 TRTHTLTRVNLE 201
   Signal
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617 AA;
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Growth factor;
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P01045;
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          TO FACTOR XII; (3) HMW-KININOGEN INHIBITS THE THROMBIN- AND PLASMIN-INDUCED AGGREGATION OF THROMBOCTES; (4) THE ACTIVE PEPTIDE BRADYKININ THAT IS RELEASED FROM HMW-KININOGEN SHOWS A VARIETY OF PHYSIOLOGICAL EFFECTS: (4A) INFLUENCE IN SWOOTH WUSCLE CONTRACTION, (4B) INDUCTION OF HYPOTENSION, (4C) NATRIURESIS AND DIURESIS, (4D) DECREASE IN BLOOD GLUCOSE LEVEL, (4E) IT IS A MEDIATOR OF INFLAMMATION AND CAUGES (4E1) INCREASE IN VASCULAR PERMEABILITY, (4E2) STIMULATION OF NOCICEPTORS (4E3) RELEASE OF OTHER MEDIATORS OF INFLAMMATION (E.G. PROSTAGLANDINS), (4F) IT HAS A CARDIOPOTECTIVE EFFECT (DIRECTLY VIA BRADYKININ ACTION, INDIRECTLY VIA ENDOTHELIUM-DERIVED RELAXING FACTOR
                                                                                                                                                            SUBCELULAR LOCATION: EXTRACELLULAR.
ALTERNATIVE PRODUCTS: HMW II AND LMW II KININOGEN PRECURSORS ARE PRODUCED FROM THE SAME GENE AS THE RESULT OF ALTERNATE MRNA SPLICING. THE SEQUENCES OF BOTH KININOGENS ARE IDENTICAL UP
                                                                                                                                                                                                                         TISSUE SPECIFICITY: PLASMA.
PTM: BRADYKININ IS RELEAGED FROM KININOGEN BY PLASMA KALLIKREIN.
SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
HELPING TO POSITION OPTIMALLY PREKALLIKREIN AND FACTOR XI NEXT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE: PS00287; CYSTATIN; 2.
Glycoprotein; Plasma; Repeat; Vasodilator; Alternative splicing;
Thiol protease inhibitor; Bradykinin; Blood coagulation; Signal;
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O-LINKED (PARTIAL).
N-LINKED (GLCNAC. .); OR 169.
N-LINKED (GLCNAC. .) (PARTIAL).
N-LINKED (GLCNAC. .).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KININOGEN, HMW II
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CYSTATIN-LIKE 1.
CYSTATIN-LIKE 2.
CYSTATIN-LIKE 3.
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BRADYKININ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00031; cystatin; 3.
PRINTS; PR0034; KININOGEN.
ProDom; PD001231; Cystatin_C_M; 1.
SMART; SM00043; Cy; 3.
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CHAIN
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
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                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AECULENCE TRYON N.A.

SUCHENCE TRYON N.A.

AEDLINE-89178677; PubMed=2926820;

AEDLINE-89178677; PubMed=2926820;

AEDLINE-89178677; PubMed=2926820;

AEDLINE-89178677; PubMed=2926820;

AEDLINE-89178677; PubMed=2926820;

AECULENCE analysis of the complete Caenorhabditis elegans myosin heavy chain gene family.";

The act of the sequence analysis of the complete Caenorhabditis elegans myosin heavy chain gene family.";

The act of the sequence analysis of the contraction.

THE AND LEGGE CONTRACTION.

THE SUBURT: MUSCLE CONTRACTION.

THE SUBURT: CALLOLAR LOCATION: Thick filaments of the myoribrils.

THE SUBURT: THE ROBLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE. SHOWING CYCLES OF A 28-RESTIONE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES.

CHOLES OF A 28-RESTIONE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES.

CHARLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

ALKYLARED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

MEROMYOSIN (LAMA) AND 1 HEAVY MEROMYOSIN (HAM). IT CAN LAFER BE SELICE TRUE.

SPLIT PURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED.
                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- MISCELLANEOUS: MHC A AND MHC B ARE FOUND EXCLUSIVELY IN THE BODY WALL MUSCLE. THEY CO-ASSEMBLE INTO BODY WALL THICK FILAMENT.
-!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
-!- SIMILARITY: CONTAINS 1 1Q DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i - MISCELLANEOUS: THERE ARE FOUR DIFFERENT MYOSIN HEAVY CHAINS IN
                                                                                                                ö
                                                                       Length 619;
                                                                                                                  Indels
154 H -> K.
68710 MW; F04320A8EB0EE0DA CRC64;
                                                                       68.3%; Score 41; DB 1; 72.7%; Pred. No. 3.1;
                                                                                                                                                                                                                                                                                                                                01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR002928; Myosin_tail.
Interpro; IPR001609; myosin_head.
Pfam; PF00612; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF00063; myosin_head; 1. PF02736; Myosin_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                           Myosin heavy chain A (MHC A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; S02771; S02771.
HSSP; P08799; 1LVK.
INCEPERO; IPR000409; IQ.
INTERPO; IPR004009; Myosin_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X08067; CAA30856.1; -.
                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
                                                                                                                                                                                            279 LNHSIAKLNAE 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBFRAGMENT (S2)
454 4
619 AA;
                                                                                                                                                       2 LTHTITKLNAE 12
                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C. ELEGANS
                                                                                                                  æ
                                                                                                                                                                                                                                                                                             MYSA_CAEEL
VARIANT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam;
Pfam;
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                                                                                                                  Matches
                                                                                                                                                                                                                                                          RESULT
  SOF
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KF4A_MOUSE
P33174;
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DOMAIN
DOMAIN
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KF4A_MOUSE
                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            090663:
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last nonotation update)
Semaphorin 3D precursor (Collapsin-2) (COLL-2).
SEMA3D OR COLL2.
Gallus gallus (Chicken).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NEUROD 14:1131-1140(1995).

-I- FUNCTION: INDUCES THE COLLAPSE AND PARALYSIS OF NEURONAL GROWTH CONES. COULD POPERATIALLY ACT AS REPULSIVE CUES TOWARD SPECIFIC NEURONAL POPULATIONS. BINDS TO NEUROPILIN.

-I- SUBCELLULAR LOCATION: Secreted.

-I- TISSUE SPECIFICITY: DEVELOPING SPINAL CORD AND DEVELOPING VISUAL SYSTEM. COLLAPSIN-1, -2, -3, AND -5 BIND TO OVERLAPPING BUT DISTINCT AXON TRACTS.

-I- DOMAIN: STRONG BINDING TO NEUROPILIN IS MEDIATED BY THE CARBOXY THIRD OF THE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                     ProDom; runocco, SMART; SM0015; IO; 1.
SMART; SM00242; NYSc; 1.
PROSITE; PS50096; IQ; 1.
Myosln; Muscle protein; Coiled coil; Thick filament; Actin-binding; APP-binding; Methylation; Alkylation; Multigene family.

MYOSIN HEAD-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDILNE-29329209; Pubmed-7605628;
Luo Y., Shepherd I., Li J., Renzi M.J., Chang S., Raper J.A.;
"A family of molecules related to collapsin in the embryonic chick
                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
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ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
W, 64577BBAF7EAD80A CRC64;
                                                                                                                                                                                                                                                                                                                                                            Score 37; DB 1; Length 1969;
Pred. No. 63;
1; Mismatches 2; Indels
                                                                                                                                                                IQ.
COILED COIL (POTENTIAL).
                                                                                                                                                                                                ATP.
ACTIN-BINDING.
ACTIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  761 AA
               PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head; 1.
                                                                                                                                                                                                                                                                                                            225509 MW;
Pfam; PF01576; Myosin_tail; 1.
                                                                                                                                                                                                                                                                                                                                                             61.78;
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                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 72.77
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                823
1969
186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1370 LTRQISKLNAE 1380
                                                                                                                                                                                                                                                                                                        1969 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                     2 LTHTITKLNAE 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             system."
                                                                                                                                                                              857
179
667
770
130
707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SM3D_CHICK
ID SM3D_CHICK
                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                            DOMAIN
DOMAIN
NP_BIND
                                                                                                                                                                                                                 DOMAIN
DOMAIN
MOD_RES
MOD_RES
MOD_RES
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InterPro; IPR003006; Ig\_MHC

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J. Cell Biol. 119:1287-1296(1992).
-!- FUNCTION: REQUIRED FOR MITOTIC CHROMOSOMAL POSITIONING AND BIPOLAR
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIPPOCAMPUS, GRANULAR CELLS IN JUVENILE CEREBELLAR CORTEX AND ADULT SPLEEN.
                                                                                                                                                                                                                   GG-LIKE C2-TYPE DOMAIN.
ARG/LYS-RICH (BASIC).
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPINDLE STABILIZATION.
--- SUBCRELULAR LOCATION: NUCLEAR, ASSOCIATED WITH MITOTIC CHROMOSOMES.
--- TISSUE SPECIFICITY: EXPRESSED IN PYRAMIDAL CELLS IN JUVENILE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECIFICITY ... SPECIFICITY ... STRAIN; STRAIN-CR; TISSUB-Brain; MEDLINE-95014709; PubMed-7929562; Sekine Y., Okada Y., Noda Y., Kondo S., Aizawa H., Takemura R., Hirokawa N.; A novel microtubule based motor protein (KIF4) for organelle transports, whose expression is regulated developmentally."; J. Cell Biol. 127:187-201(1994).
                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                 Pfam; PF00047; ig; 1.
Pfam; PF01403; Sema; 1.
SMART; SW00410; II, S.
SMART; SW00423; PSI; 1.
Signal; Immunoglobulin domain; Multigene family; Neurogenesis; Developmental protein; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, AND TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. CHROMOKINESIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                60.0%; Score 36; DB 1; Length 761; 70.0%; Pred. No. 35; 3; Indels ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Brain;
MEDLINE-93077686; PubMed-1447303;
Alzawa H., Sekine Y., Takemura R., Zhang Z., Nangaku M.,
Hirokawa N.,
                                                                                                                                                                                                                                                                                                  LINKED (GLCNAC. . .) (POSE 3E09AE3DBA53F46B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1993 (Rel. 27, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Chromosome associated kinesin KIF4A (Chromokinesin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1231 AA
                                                                                                                                                                                   SEMAPHORIN 3D.
                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                       SEMA.
Ig_like.
PSI.
                                                                                                                                                                                                                                                                                                               87300 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 91-240 FROM N.A.
   InterPro; IPR003600; Ig_11]
InterPro; IPR003659; PSI.
InterPro; IPR001627; Sema.
                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                      543
726
757
719
127
595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KIF4A OR KIF4 OR KNS4.
                                                                                                                                                                                     255
245
646
727
727
127
127
595
595
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| 659 TFIHTIVKEN 668
                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TLTHTITKLN 10
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HSLV_XYLFA
           KESULT 11
HSLV_XYLFA
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                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 17.2 kDa protein in MELC2-RNHH intergenic region (ORF3). Streptomyces lincolnensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                               Score 36; DB 1; Length 1231;
Pred. No. 58;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.3%; Score 35; DB 1; Length 150; 60.0%; Pred. No. 9.4; 1:ve 2; Mismatches 2; Indels
                                                                                                                                                                                                     COILED COIL (BY SIMILARITY)
                                                                                                                                                                                                                                   > S (IN REF. 2).
F34F2C2D21158FE4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhang H.Z., Plepersberg W.;
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
                                                                          HSSP, P17119; 3KAR.
MGD; MGI:108389; Kife.
MGD; MGI:108389; Kife.
Pfam; PF00225; Kinesin; 1.
PRINTS; PR00380; KINESINIEAVY.
SMART; SM00129; KISC; 1.
PROSITE; PS00411; KINESINIMOTOR_DOMAIN1; 1.
PROSITE; PS06067; KINESINIMOTOR_DOMAIN2; 1.
MGCOS protein; Microtubules; ATP-binding; DNA-binding; Nuclear protein; Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       al protein.
150 AA; 17167 MW; 4F9B48B727D3967F CRC64;
                                                                                                                                                                                                              GLOBULAR.
ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                        150 AA.
                                                                                                                                                                                         KINESIN-MOTOR
                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                             1231 AA; 139551 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996 (Rel. 34, Created)
                                                                                                                                                                                                                                                                               60.0%;
                                                     EMBL; D12646; BAA02167.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X95703; CAA65001.1; -.
                                                                                                                                                                                                                                                                              Query Match 60.0
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                             1231
95
112
                                                                PIR; D44259; D44259.
                                                                                                                                                                                                                                                                                                                                                632 HTVSKLNOE 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TLIHTITKEN 10
                                                                                                                                                                                                                                                                                                                          4 HTITKLNAE 12
                                                                                                                                                                                                  351
1001
88
112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=78-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical
SEQUENCE 15
                                                                                                                                                                                                                                                                                                                                                                                                    YMEL_STRLN
P55049;
                                                                                                                                                                                                                      NP_BIND
CONFLICT
SEQUENCE
                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                              DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                 EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - COMPLIANT ENDING TO STATE THE COMPLEX (BY SIMILARITY).
- COMBUNI: INTERACTS WITH HGLU (BY SIMILARITY).
- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
- SIMILARITY: BELONGS TO PEPTIDASE FAMILY T1B; ALSO KNOWN AS THE PROTEASOME B-TYPE FAMILY. HSLV SUBFAMILY.
                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the Swiss Institute of Bioinformatics and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase, Protease, Complete proteome.

ACT_SITE 8 B BY SIMILARITY.

SEQUENCE 178 AA, 18803 MW; A4406BED1A3275EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 35; DB 1;
                                              kel. 40, Last sequence update)
kel. 41, Last annotation update)
protease hslv (EC 3.4.25.-).
178 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.
 PRT;
                                                                                                                                                                                                                                        MEDLINE=20365717; Pubmed=10910347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001353; Proteasome.
                                 (Rel. 40, Created)
(Rel. 40, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE003978; AAF84293.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
'-hos 7; Conserva
                                                                                                   HSLV OR XF1484.
Xylella fastidiosa
                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                   (Rel.
                                                                                                                                                                        NCBI_TaxID=2371;
                                                                                     ATP-dependent
                                                                   01-MAR-2002
                                 16-OCT-2001
                                                   16-OCT-2001
                                                                                                                                                                                                                        STRAIN=9A5C
                                                                                                                                                        xylella
                 09PD95;
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1 TLTHTITKLNA 11

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| | | | | : | : | 43 TLTHWVTSVN 52

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STRAIN-BUFFALO;
                     SEQUENCE F
                                                                                                                                                                                    SEQUENCE
  Biol.
  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                             U1-AUG-1992 (Rel. 23, Last sequence update)
O1-AUG-1992 (Rel. 23, Last annotation update)
Coat protein (Capsid protein).
Lily symptomless virus (LSV).
Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
VCBI_TAXID=12173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS HMW AND LMW).
MEDLINE-87137443; PubMed-3029068;
Kitagawa H., Kitamura N., Hayashida H., Miyata T., Nakanishi S.;
"Differing expression patterns and evolution of the rat kininogen
                                                                                                                                                                                               symptomless
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                    Length 291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                           -1- SIMILARITY: TO THE COAT PROTEINS FROM POTEXVIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                             291 AA; 32041 MW; 57E289F3EA726388 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                         58.3%; Score 35; DB 1; 72.7%; Pred. No. 19; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KNG_RAT STANDARD; PRT; 639 AA. P08934; P08933; 01-NOV-1988 (Rel. 09, Created) 10-NOV-1988 (Rel. 09, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Kininogen precursor [Contains: Bradykinin].
                                                          291 AA
                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000052; Potex_carlavirus_coat. Pfam; PF00286; virus_P-coat; 1. PRINTS; PR00232; POTXCARLCOAT.
                                                                                                                                                                                                                                                                                                                                                                              Probom; PD000603; Potex_carlavirus_coat; 1.
PROSITE; PS00418; POTEX_CARLAVIRUS_COAT; 1.
                                                          PRT;
                                                                                                                                                                                                                                                                                                                                             EMBL; X15343; CAA33401.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
28 TLGHTVMKSNA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 LTHTITKLNAE 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           || | ||||||
46 LTRLIEKLNAE 56
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 8; Conserv
                                                                           01-AUG-1992 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qene family."
                                                                                                                                                                                                                                                                                                                                                                                                     Coat protein
SEQUENCE 2
                                                        COAT_LSV
P27335;
                                      12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
                                                 COAT_LSV
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                                      RESULT
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**Rageyama R., Kitamural.oliable)**

**Rageyama R., Kitamural o. Ohkubo H., Nakanishi S.;

**Rageyama R., Kitamural o. Ohkubo H., Nakanishi S.;

**Tolifering utilization of homologous transcription initiation sites

**Tolifering utilization of the propertion of the p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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ALTERNATIVE PRODUCTS: 2 ISOFORNS; HWM (SHOWN HERE) AND LMW; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: PLASMA.
PTM: BRADYKININ IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN.
MISCELLANEOUS: RAT EXPRESS FORM TYPES OF KININOGENS: THE CLASSICAL HWW/LMW KININOGENS AND THO ADDITIONAL LMW-LIKE KININOGENS: T'I AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-87250580; PubMed-2439509;
MEDLINE-87250580; PubMed-2439509;
Structure and expression of the genes for major acute phase alpha 1-protein (thiostatin) and kininogen in the rat.";
J. Biol. Chem. 262:9298-9308(1987).
                                                                                                                                                                                                                       Furuto-Kath S., Matsumoto A., Kitamura N., Nakanishi S.; "Primary structures of the mRNAs encoding the rat precursors for bradykinin and T-kinin. Structural relationship of kininogens with
                                                                                                                                                                                                                                                                                                                                                                                     major acute phase protein and alpha 1-cysteine proteinase inhibitor (;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biol. Chem. 260:12054-12059(1985).
dhem. 262:2190-2198(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000010; Cystatin.
InterPro; IPR00243; Cystatin_C_M.
InterPro; IPR002395; Kininogen.
Pfam: PF00031; Cystatin; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M11884; AAA41487.1; -.
BMBL; M14569; AAA41484.1; -.
EMBL; M14569; AAA41485.1; ALF_SEQ.
EMBL; M16455; AAA41482.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-WISTAR; TISSUE-Liver;
MEDLINE-87137465; PubMed-3818598;
                                                                                                                                                                               PubMed-2413018;
                                                                                                                    ROM N.A. (LMW ISOFORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L29428; AAA41486.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-65 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OF 1-41 FROM N.A.
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PIR; A28055; A28055.
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Query Match
Best Local Similarity
Matches 7; Conserv
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SEQUENCE
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ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: (1) KININOGENS ARE INHIBITORS OF THIOL PROTEASES; (2)
HUM-KININOGEN PLAYS AN IMPORTANT ROLE IN BLOOD COAGULATION BY
HELPING TO POSITION OPTIMALLY PREKALLIKREIN AND FACTOR XI NEXT TO
FACTOR XII; (3) HUM-KININOGEN INHIBITS THE THROMBIN-AND PLASMIN-
INDUCED AGGREGATION OF THROMBOCYTES; (4) THE ACTIVE PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                          SMART; SM00043; CY; 3.
PROSITE; PS00287; CYSTATIN; 2.
Glycoprotein; Plasma; Repeat; Thiol protease inhibitor; Vasodilator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VSPSYIARVQEERDPGNEQGPIHGHGWLHAKQ -> RLL1
CEYKGRLLKAGAGPAPERQAEASTVTP (IN ISOFORM
                                                                                                                                                                                                                                                                 BY SIMILARITY.
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N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6 x CBA; TISSUE=Liver;
Takano M., Kondoh J., Yayama K., Okamoto H.;
"Molecular cloning of cDNAs for mouse low- and high- molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
                                                                     Bradykinin; Blood coagulation; Inflammatory response; Signal; Alternative splicing; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58.3%; Score 35; DB 1; Length 639; 63.6%; Pred. No. 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                         INTERCHAIN (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MISSING (IN ISOFORM LMW).
E -> K (IN REF. 2).
D3172DF94FF56AF5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                              (GLCNAC. . .) (
GLCNAC. . .) (
GLCNAC. . .) (
                                                                                                                                           KININOGEN HEAVY CHAIN.
                                                                                                                                                                         KININOGEN LIGHT CHAIN.
CYSTATIN-LIKE 1.
CYSTATIN-LIKE 2.
CYSTATIN-LIKE 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KNG_MOUSE STANDARD; PRT; 661 AA. 008677; 008676; 16-0CT-2001 (Rel. 40, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update) Kininogen precursor [Contains: Bradykinin].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 45;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORMS HMW AND LAWW).
                                                                                                                                                          BRADYKININ.
                                                                                                                                                                                                                                        HIS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED
              PD001231; Cystatin_C_M; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
70933 MW;
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                                                                                                                                                                                                                                                                                                                                                                    340
370
82
1127
1169
205
205
529
433
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282 LGHSIAQLNAE 292
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639 AA;
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                          kininogen.";
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CARBOHYD
VARSPLIC
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CONFLICT
SEQUENCE
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              ProDom; |
SMART; SI
                                                                                                                                                          PEPTIDE
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KNG_MOUSE
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NAME OF THE PET OF THE
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BRADYKININ THAT IS RELEASED FROM HWW-KININGGEN SHOWS A VARIETY OF
COUTRACTION, (4B) INDUCTION OF HYPOTENSION, (4C) NATRITRESIS AND
COUTRACTION, (4B) INDUCTION OF HYPOTENSION, (4C) NATRURESIS AND
DIURESIS, (4D) DECREASE IN BLOOD GLUCOSE LEVEL, (4E) IT IS A
MEDIATOR OF INFLAMMATION OF NOCICEPTORS (4E) TELEASE OF
COTHER MEDIATORS OF INTLAMMATION OF NOCICEPTORS (4E) THAS
COTHER MEDIATORS OF INTLAMMATION OF NOCICEPTORS (4E) THAS
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COLOTTING SOURTHAST TO HWW-KININGEN NOT INVOLVED IN BLOOD
COLOTTING SOURTHAST TO HWW-KININGEN NOT INVOLVED IN BLOOD
COLOTTING SOURTHAST TO HWW-KININGEN NOT INVOLVED IN BLOOD
COLOTTING SOCIETED
COLOTTING SOURTHAST SOURCE (4G)
COLOTTING SOURCE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PRINTS; PR00034; KININOGEN.
PPODOM: PD001221; Cystatin_C_M; 1.
SMART; SM00043; CY; 3.
PROSITE; PS00287; CYSTATIN; 1.
BROSITE; PS00287; CYSTATIN; Thiol protease inhibitor; Vasodilator;
Bradykinin; Blood coagulation; Inflammatory response; Signal;
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EMBL; D84415; BAA19742.1; -.
MGD; MGI:1097705; Kng.
InterPro; IPR0000010; Cystatin.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-5286. / AB972;
Badcock K., Churcher C.M., Barrell B.G., Rajandream M.A.;
Bubmitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Alpha, alpha-trehalose + H(2)0 = 2 D-glucose.
-!- SUBCELLUIAR LOCATION: LYSOSOME-LIKE VACUOLES (POTENTIAL).
-!- SIMILARITY: BELONGS TO FAMILY 65 OF GLYCOSYL HYDROLASES.
-!- SIMILARITY: BELONGS TO FAMILY 65 OF GLYCOSYL HYDROLASES.
-!- AMBL outst
                                                                                                                                                                                                    MEDLINE-96076626, PubMed-7502577;
Destruelle M., Holzer H., Klionsky D.J.;
"Isolation and characterization of a novel yeast gene, ATH1, that is required for vacuolar acid trehalase activity.";
yeast 11:1015-1025(1995).
                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                        01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Vacuolar acid trehalase precursor (EC 3.2.1.28) (Alpha, alpha-trehalase) (Alpha-trehalase glucohydrolase).
ATHI OR YPR026W OR YP9367.06.
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EMBL; Z49274; CAA89280.1; -.
EMBL; Z71255; CAA95022.1; -.
EMBL; X71255; AA95022.1; -.
Hydrolase; Glycosidase; Glycoprotein; Signal.
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136920 MW; 34AEC44BOB64BDEC CRC64;
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Mammalia; Euthéria; Primates; Catarrhini; Hominidae; Homo.
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"The sequence of Homo sapiens PAC clone RP4-747G18.";
Submitted (JUM-1998) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=99093792; PubMed=9847074;
Sulston J.W., Waterston R.'
Toward a complete human genome sequence.";
Genome Res. (8:1097-1108(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM
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SEQUENCE
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Q6883 hepatitis c
Q9qix4 hepatitis c
Q9qix3 hepatitis c
Q03884 saccharomyc
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                                                                              July 1, 2002, 16:29:44; Search time 75.26 Seconds (without alignments)
27.584 Million cell updates/sec
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            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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PRINTS; PR00508; S21N4MTFRASE.
7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-98000940; PubMed-9344675; Canu N., Possenti R., Ricco A.S., Rocchi M., Levi A.; Canu N., Possenti R., Ricco A.S., Rocchi M., Levi A.; "Cloning, structural organization analysis and chromosomal assignment of the human gene for neurosecretory protein VGF."; Genomics 45:443-446(1997).

EMBL; Y12661; CAA73210.1; -. SEQUENCE 616 AA; 67286 MW; CD1920610201BEB9 CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Appl. Environ. Microbiol. 65:2015-2019(1999).
-!- SIMILARITY: BELONGS TO THE CRP/FNR FAMILY OF TRANSCRIPTIONAL REGULATORS.
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Rhizobiaceae; Rhizobium.
NCBL_TaxID-29449;
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                                                                                                                                           015240 PRELIMINARY; PRT; 616 AA.
015240;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEURO-ENDOCRINE SPECIFIC PROTEIN VGF.
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Pred. No. 14;
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SEQUENCE 265 AA; 29277 MW; DA90B06
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01-MAY-1997 (TrEMBLrel. 03, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last anno
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InterPro; IPR000595; cNMP_binding.
InterPro; IPR01808; HTH_CRP.
Pfam; PF00027; cNMP_binding; 1.
Pfam; PF00325; crp; 1.
SMART; SM00100; cNMP; 1.
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77.8%;
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187 TRTHTLTRVNLE 198
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Best Local Similarity
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PubMed=10223993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The genome sequence of the plant pathogen Xylella fastidiosa.";
Nature 406:151-159(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60730 MW; 3B429E738DB4E699 CRC64;
                                                                                                   01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
534 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE004016; AAF84770.1; -. InterPro; IPR002295; D21N6_mtfrase. InterPro; IPR001091; N4_Mrase. InterPro; IPR002052; N6_Mtase. InterPro; IPR002941; N6_Mtase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20365717; PubMed=10910347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | | : |||||
359 TTAHAVAKLNAE 370
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Nagayama K., Kurosaki M., Enomoto N., Maekawa S.y., Miyasaka Y.,
Tazawa J.i., Izumi N., Marumo F., Sato C.;
"Time-related changes in full-length hepatitis C virus and hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PD186062; HCV_NSI; 1.
ATP-binding; Coat protein; Envelope protein; Glycoprotein; Helicase;
Nonstructural protein; Polyprotein; RNA-directed RNA polymerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DRC-2001 (TrEMBLrel. 19, Last annotation update)
GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E2 (GP68) (GP70)
Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                              Nagayama K., Kurosaki M., Enomoto N., Maekawa S., Miyasaka Y., Sakamoto N., Fukuma T., Tazawa J., Izumi N., Marumo F., Sato C.; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

-- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN E1. EPRE., AF165601; AAD56196.1; -. MEROPS; S29.001; -. MEROPS; U39.001; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 3010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3010 AA; 327386 MW; 94C94662C44A7695 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 39; DB 12;
Pred. No. 1.8e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3010 AA
                                                                             SEQUENCE FROM N.A.
STRAIN-MD9-1;
MEDLINE-20013325; PubMed=10544098;
                                                                                                                                                                                                                                                                                                                                                                                                        HCV_capsid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002868; HCV_NSSa.
InterPro; IPR002166; HCV_RORP.
InterPro; IPR001650; Helicase_O
Pfam; PF01543; HCV_capsid; 1.
Pfam; PF01539; HCV_core; 1.
Pfam; PF01539; HCV_core; 1.
Pfam; PF01560; HCV_NSI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65.0%;
88.9%;
                                                                                                                                                                                 activity.";
Virology 263:244-253(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01506; HCV_NS5a; 1.
Pfam; PF00998; HCV_RdRP; 1.
Pfam; PF00271; helicase_C;
                                                                                                                                                                                                                                                                                                                                                                                         DEAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF02907; HCV_NS3; 1
PF01006; HCV_NS4a; 1
PF01001; HCV_NS4b; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF01538; HCV_NS2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro; IPR002531; H
Interpro; IPR002518; H
Interpro; IPR004109; H
Interpro; IPR000745; H
                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR001490;
                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002522;
                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |||| ||||
1636 TLTHPITKL 1644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NS1)].
Hepatitis C virus.
                                             NCBI_TaxID=11103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TLTHTITKL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane
                                                                                                                                                                                                                                            STRAIN=MD9-1;
                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09QIX3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0901X3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00271; helicase_C; 1.
ProDom; PD186062; HCV_NS1;
ATP-binding; Coat protein; Envelope protein; Glycoprotein; Hellcase; Nonstructural protein; Polyprotein; RNA-directed RNA polymerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  090IX4 PRELIMINARY; PRT; 3010 AA.
090IX4;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E2 (GP68) (GP70) (NS1)].
                                                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E2 (GP68) (GP70)
                                                                                                                                                                                                                                                                         Cho J.M., Park Y.-W., Lee Y.-B., Yang J.-Y., Kim C.-H., Choo S.-H., Ryu W.-S.,
"Molecular cloning of hepatitis C virus genome from a single Korean
                                                                                                                                                                    Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 3010;
                                                                                                                                                                                                                                                                                                                        blood donor.;
Mol. Cells 5:317-324(1995).
Mel. Cells 5:317-324(1995).
Mel. Gullahrity: TO HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN HSSP; P26663; LJyrp.
InterPro; IPR001410; DEAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3010 AA; 326855 MW; 455BA4BF8CEF210E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 39; DB 12;
Pred. No. 1.8e+02;
); Mismatches 1;
                                                  PRT; 3010 AA
                                                                                                                                                                                                                                                                                                                                                                                                                       HCV_capsid.
HCV_core.
HCV_env.
HCV_NSI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR001490; HCV_NS4b.
IPR002868; HCV_NS5a.
IPR002166; HCV_RGRP.
IPR001650; Helicase_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fam; PF01543; HCV_capsid;
fam; PF01542; HCV_core; 1.
fam; PF01539; HCV_env; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HCV_NS4b; 1.
HCV_NS5a; 1.
HCV_RdRP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HCV_NS1; 1.
HCV_NS2; 1.
HCV_NS3; 1.
HCV_NS4&; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |||| ||||
1636 TLTHPITKL 1644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                               Hepatitis C virus.
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                              NCBI_TaxID=11103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TLTHTITKL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF01006;
                                                                                                                                                                                                                                                               STRAIN-HCV-L2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF02907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane
SEQUENCE 30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
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                    RESULT
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E2 (GP68) (GP70)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                    Length 268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63.3%; Score 38; DB 3; Length 498; 72.7%; Pred. No. 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=AB972;
Barrell B., Rajandream M.A.;
Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; Z46727; CAA86685.1; ...
SGD; S0002887; YDR179W-A.
Hypothetical protein.
SEQUENCE 498 AA; S7916 MW; 60959427D7A230CD CRC64;
                                                                                                                                       STRAIN-AB972;
Barrell B., Rajandram M.A.;
Barrell B., Rajandram M.A.;
Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; 246727; CAA86686.1; -
SGD; S0002887; YDR179W-A.
Hypothetical protein.
SEQUENCE 268 AA; 31096 MW; 45C7F756F361C71D CRC64;
                                                                         Murphy L., Harris D.E., Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murphy L., Harris D.E.;
Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
 Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 57.9 KDA PROTEIN.
                                                                                                                                                                                                                                                                                 63.3%; Score 38; DB 3; 72.7%; Pred. No. 23; cive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            498 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 3010 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                 Query Match 63.3
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 63.3
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                   || | |:||||
144 TLQHWISKLNA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     || | |:||||
374 TLQHWISKLNA 384
                                                                                                                                                                                                                                                                                                                                               1 TLTHTITKLNA 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TLTHTITKLNA 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                           SEQUENCE FROM N.A.
                                               SEQUENCE FROM N.A.
                NCBI_TaxID=4932;
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                                                               STRAIN-AB972;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           003983
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Q9QIX8
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                                                                                                         Nagayama K., Kurosaki M., Enomoto N., Maekawa S.y., Miyasaka Y.,
Tazawa J.i., Izumi N., Marumo F., Sato C.;
"Time-related changes in full-length hepatitis C virus and hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01538; HCV_NS3; 1.
Pfam; PF01907; HCV_NS3; 1.
Pfam; PF01900; HCV_NS4; 1.
Pfam; PF01001; HCV_NS4; 1.
Pfam; PF01098; HCV_NS5; 1.
Pfam; PF00998; HCV_RRP; 1.
Pfam; PF00998; HCV_RRP; 1.
ATP-binding; Coat protein; Envelope protein; Glycoprotein; Helicase; Nonstructural protein; Polyprotein; RNA-directed RNA polymerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                Nagayama K., Kurosaki M., Enomoto N., Maekawa S., Miyasaka Y., Sakamoto N., Fukuma T., Tazawa J., Izumi N., Marumo F., Sato C.; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-1 - SIMILARITY: TO HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN E1. EMBL; AP165062; AAD56197.1; -. VIRUS ENVELOPE GLYCOPROTEIN E1. HSSP: P26663; INS3.
MEROPS: S29.001; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         003984 PRELIMINARY; PRT; 268 AA.
003984; OLINOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 16, Last annotation update)
4PPOTHETICAL 31.1 KDA PROTEIN.
YOR179W-A.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 65.0%; Score 39; DB 12; Length 3010; Best Local Similarity 88.9%; Pred. No. 1.8e+02; Matches 8; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3010 AA; 327253 MW; 9F1B0B3F536774FA CRC64;
                                                                          STRAIN=MD9-2;
MEDLINE=20013325; PubMed=10544098;
                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002519; HCV_env.
InterPro; IPR002511; HCV_env.
InterPro; IPR002518; HCV_NS2.
InterPro; IPR001409; HCV_NS2.
InterPro; IPR001409; HCV_NS4a.
InterPro; IPR001409; HCV_NS4b.
InterPro; IPR002868; HCV_NS5a.
InterPro; IPR002166; HCV_RS5a.
InterPro; IPR00166; Helicase_C.
                                                                                                                                                                                                                                                                                                                                                                            HCV_core.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01543; HCV_capsid; 1. Pfam; PF01542; HCV_core; 1. Pfam; PF01539; HCV_env; 1. Pfam; PF01560; HCV_NS1; 1.
                                                                                                                                                                       Virology 263:244-253(1999).
                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001410; DEAD.
InterPro; IPR002522; HCV_c
                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002521;
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1636 TLTHPITKL 1644
                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                             SEQUENCE FROM N.A.
                           NCBI_TaxID=11103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TLTHTITKL 9
                                                                                                                                                                                                                       STRAIN-MD9-2;
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                                                                                                                                                       activity.
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Q03984
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Gaps

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ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                              HCV_core.
HCV_core.
HCV_env.
HCV_NSI.
                                                                                                                                                                                                                                                                                                                                                                                                                           helicase_C; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.3%;
ilarity 77.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                               PF01539, HCV_env, 1.
PF01560; HCV_NS1; 1.
PF02907; HCV_NS3; 1.
PF01006; HCV_NS4s; 1.
PF01001; HCV_NS4s; 1.
PF07566; HCV_NS5s; 1.
PF07566; HCV_RS5s; 1.
                                                                                                           Virology 263:244-253(1999).
                                                                                                                                                                                                                     InterPro; IPR001410; DEAD.
InterPro; IPR002522; HCV_c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                 InterPro; IPR002519;
                                                                                                                                                                                                                                                          InterPro; IPR002531;
                                                                                                                                                                                                                                        InterPro; IPR002521;
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1636 TLTHPVTKL 1644
         Viruses: ssRNA posi
Hepacivious
NCBI_TaxID=11103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                              SEQUENCE FROM N.A.
                                              SEQUENCE FROM N.A.
 Hepatitis C virus
                                                                                                                                                                                                   MEROPS; S29.001;
MEROPS; U39.001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane
                                                        STRAIN=MD7-;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    084895
084895;
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084895
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                                                                                Nagayama K., Kurosaki M., Enomoto N., Maekawa S.y., Miyasaka Y.,
Tazawa J.i., Izumi N., Marumo F., Sato C.;
"Time-related changes in full-length hepatitis C virus and hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                        Probom; PD186062; HOV_NSI; 1.
ATP-binding; Coat protein; Envelope protein; Glycoprotein; Helicase;
Nonstructural protein; Polyprotein; RNA-directed RNA polymerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GENOME POLYPROTEIN (CONTAINS: ENVELOPE GLYCOPROTEIN E2 (GP68) (GP70)
         Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3010 AA; 326986 MW; 55F505A208C6E5CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 38; DB 12;
Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 3010 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                      MEDLINE-20013325; PubMed-10544098;
                                                                                                                                                                                                                                                                                          IPRO00745; HCV_NS4a.
IPRO01490; HCV_NS4b.
IPRO02868; HCV_NS5a.
IPRO0166; HCV_RGRP.
IPRO01650; Hellcase_C.
                                                                                                                                                                                                                                      HCV_capsid.
                                                                                                                                                                                                                                                                                                                                        fam; PF01543; HCV_caps1d; 1.
fam; PF01542; HCV_core; 1.
                                                                                                                                                                                                                                                                                                                                                                                                               HCV_NS5a; 1.
HCV_RdRP; 1.
helicase_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.3%;
                                                                                                        activity.";
Virology 263:244-253(1999).
                                                                                                                                                                                                                                                                                                                                                          HCV_env; 1.

HCV_NS1; 1.

HCV_NS2; 1.

HCV_NS3; 1.

HCV_NS4a; 1.

HCV_NS4a; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 77.۰۰
آب Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                IPR002531;
IPR002518;
                                                                                                                                                                                                                                                                                  IPR004109;
IPR000745;
                                                                                                                                                                                                                             InterPro; IPR001410;
                                                                                                                                                                                                                                                                                                                       InterPro; IPR002166;
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1636 TLTHPVTKL 1644
                                                                                                                                   SEQUENCE FROM N.A.
                                   NCBI_TaxID=11103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TLTHTITKL 9
                                                                                                                                                                                                          MEROPS; S29.001;
MEROPS; U39.001;
                                                                                                                                                                                                                                                                                                                                                                                             PF01006;
                                                                                                                                                                                                                                                                                                                                                                                                                       PF00998;
                                                                                                                                              STRAIN-MD7-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fransmembrane
                                                              STRAIN-MD7-1
                                                                                                                                                                                                                                                                 InterPro;
InterPro;
                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                         InterPro;
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0901X7;
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                                                                                                                                                                                                                                                                                                                                                  Pfam;
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DELLE
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MEDLINE-20013325; PubMed-10544098; Nackawa S.y., Miyasaka Y., Nagayama K., Kurosaki M., Enomoto N., Mackawa S.y., Miyasaka Y., Tazawa J.i., Izumi N., Marumo F., Sato C.; "Time-related changes in full-length hepatitis C virus and hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probom; PD186062; HCV_NSI; 1.
ATP-binding; Coat protein; Envelope protein; Glycoprotein; Helicase;
Nonstructural protein; Polyprotein; RNA-directed RNA polymerase;
                                                                                                                                                                                                                               STRAIN-MD7-2; Rurosaki M., Enomoto N., Maekawa S., Miyasaka Y., Nagayama A., Furosaki M., Enomoto N., Maekawa S., Miyasaka Y., Sakamotoja M., Fukuma T., Tazawa J., Izumi N., Marumo F., Sato C.; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases. - I- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN E1. EMBL, AF165058; AAD56193.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
NYPOTHETICAL 11.3 KDA PROTEIN.
Salmonella typhimurium.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3010 AA; 326974 MW; A3556D74F0C3AD2B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 38; DB 12;
Pred. No. 2.7e+02;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002518; HCV_NS2.
InterPro; IPR004109; HCV_NS3.
InterPro; IPR001490; HCV_NS4a.
InterPro; IPR001868; HCV_NS5a.
InterPro; IPR0021868; HCV_NS5a.
InterPro; IPR002186; HCV_RGAP.
InterPro; IPR001650; Helicase_C.
Pfam; PP01543; HCV_Capsid; 1.
Pfam; PP01543; HCV_Core; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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Eukaryota; Merazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unkmeir A., Schmidt H.;

Structural analysis of phage-borne stx genes and their flanking sequences in shiga toxin-producing escherichia coli and shigella dysenteriae typel strants.";

Infect. Immun. 68:4856-4864(2000).

BMBL; AJ271139; CAC05572.1;

Hypothetical protein.

SEQUENCE 60 AA; 7199 MW; 37845BB5F08D1EFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1992;
                                                                                                                                                                          'Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 37; DB 5; Length 199
Pred. No. 2.8e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 60;
                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00015; IQ; 1.
SMART; SM00242; MYSc; 1.
SEQUENCE 1992 AA; 228362 MW; 8676AA34DAD7E835 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                           Harris B.R.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 7.2 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
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Pred. No. 12;
1; Mismatches
                                                                                                                                                                                                                                       InterPro; IPR0010048; IQ.
InterPro; IPR001609; myosin_head.
InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail.
Pfam; PF00612; IQ; 1.
Pfam; PF0063; myosin_head; 2.
Pfam; PF01776; Myosin_tail: 1.
Pfam; PF01776; Myosin_tail: 1.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=H.I.8.;
MEDLINE=20407286; PubMed=10948097;
                                                                                                                                              MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                            61.78;
72.78;
                                                                                                                                                                                      investigating biology.";
Science 282:2012-2018(1998).
EMBL; Z78199; CABO1576.1; --
HSSP; PO8799; IMND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60.0%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 72.،،
ادم 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 60.0
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
 K12F2.1.
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | | |:|||||
1393 LTRQISKLNAE 1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 LTHTITKLNAE 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TLTHTITKLN 10
                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=562;
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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                                                                                                                                                                          Length 103;
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                                                                                                                                                                                                   3; Indels
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                                                            Figueroa-Bossi N., Bossi L.;
Prophage genes in Salmonella.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF001386; AAC26074.1; -.
Hypothetical protein.
SEQUENCE 103 AA; 11325 MW; 84379F22D7906527 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Coles L.; Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001930; Aladiptase.
InterPro; IPR00130; Zn_MTpeptdse.
Pfam; PF01433; Peptidase_M1; 1.
PRINTS; PR00756; ALADIPTASE; UNKNOWN 1.
SEQUENCE 786 AA; 90448 MW; CAAIACD3A1803C9A CRC64;
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Pred. No. 13;
2; Mismatches
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MEDLINE-99069613; PubMed-9851916;
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Q21440;
Q1-NOV-1996 (TrEMBLrel. 01, C.
G1-NOV-1996 (TrEMBLrel. 01, L.
O1-DEC-2001 (TrEMBLrel. 19, L.
K12F2.1 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     investigating biology.";
Science 282:2012-2018(1998).
EMBL, 269794; CAA93681.1; -.
MEROPS; MOI.UPW; -.
                                                                                                                                                                         61.7%;
58.3%;
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                                                                                                                                                                       Query Match 61.7
Best Local Similarity 58.3
Matches 7; Conservative
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44 TLAHTVEKRDAE 55
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             NCBI_TaxID=602;
                                                    STRAIN-LT2;
Salmonella
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Q21673
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Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum

Listing first 45 summaries

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Database

Match 100%

747574 seqs, 111073796 residues

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Searched:

1 TLTHTITKLNAE 12 US-09-461-061A-2 60

Title: Perfect score:

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Novel human diagno
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Miniature swine re
Retoviral protein
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Drosophila melanog
HCV polypeptide 9.
Hepatitis C virus
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glutamicum prote
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Drosophila melanog
Human ORFX ORF1707
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Human foetal prote
Human foetal prote
               Human polypeptide
Anti-angiogenic D3
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Hepatitis C virus
HCV polypeptide 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anti-angiogenic peptide N-terminal fragment.
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                                     AAB54127
AAM06387
AAM06833
                                                                                                         AAU53927
ABB60240
AAB41943
ABG09135
ABG10240
ABG14540
ABG19900
AAW32097
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AAY95409
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AAG91497
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AAO00443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY95406 standard;
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RESULT
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| SIDS1/gcddata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
| SIDS1/gcddata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
| SIDS1/gcddata/hold-geneseqy-embl/AA1981.DAT:*
| SIDS1/gcddata/hold-geneseqy-embl/AA1981.DAT:*
| SIDS1/gcddata/hold-geneseqy-embl/AA1981.DAT:*
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| SIDS1/gcddata/hold-geneseqy-embl/AA1990.DAT:*
                                                                                        July 1, 2002, 16:19:43; Search time 95.97 Seconds (without alignments) 13.889 Million cell updates/sec
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Description	Anti-andiodenic pe	Anti-angiogenic D3	Domaine 3, bradyki	Human kininogen D3	Human high mol.wt.	Novel human diagno	Novel human diagno	Novel human diagno	Novel human diagno	Bradykinin protein	Bradykinin protein
SUMMARIES	AAY95406	AAY95408	AAR33350	AAB37447	AAY95426	ABG21102	ABG21099	ABG21105	ABG21101	AAP40257	AAP40633
DB	21	21	14	21	21	22	22	22	22	ß	S
% Query e Match Length DB	12	32	117	122	123	248	369	435	644	436	434
å Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	70.0	68.3
Score	9	9	09	9	9	09	9	09	9	42	41
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rheumatoid arthritis, and ocular disorders comprises a kininogen domain
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                                                                             The present sequence is that of an N-terminal fragment of a novel anti-angiogenic D3 peptide (see AAY95408) derived from human high mol.wt. Kinlogen (HX) domain 3 (see AAY95406). The tull-length D3 peptide inhibits endothelial cell proliferation and thus possesses anti-angiogenic activity. It is an example of peptides of the invention (see AAY95405-26) that are analogues of certain sites in the HX domain 3. The peptides inhibit endothelial cell proliferation and may also induce endothelial cell apoptosis. Compositions including the peptides are used in claimed methods for inhibiting angiogenesis, inhibiting endothelial cell proliferation, and inducing endothelial cell propposis. Cancer, rheumatoid arthritis, and ocular disorders characterized by undesired vascularization of
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is that of a D3 peptide derived from human high mol.wt. kininogen (HK) domain 3 (see AAY95426). The D3 peptide inhibits endothelial cell proliferation and thus possesses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anti-angiogenic; angiogenesis; inhibitor; kininogen; homologue; andothelial cell proliferation; apoptosis; cancer; ocular disorder; rheumatoid arthritis; cytostatic; antiarthritic; antirheumatic; therapy; human; D3 peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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                                                 Claim 3; Page 25; 44pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                            the retina are treated.
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Matches 12; Conserv
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                   3 analog
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Domain 3; human; kininogen; heavy chain; low molecular weight; plasma; trypsin; platelet; activation; granule contents; hemostasis; thrombin; tissue plasminogen activator; thrombosis; inflammatory response;
                                                                                                                                                                                                                                                                         Gaps
                                                                    induce endothelial cell apoptosis. Compositions including the peptides are used in claimed methods for inhibiting angiogenesis, inhibiting endothelial cell proliferation, and inducing endothelial cell proliferation, and inducing endothelial cell apoptosis. Cancer, rheumatoid arthritis, and ocular disorders characterized by undesired vascularization of the retina are treated.
anti-angiogenic activity. It is an example of D3 peptides of the invention (see AAV95405-26) that are analogues of certain sites in the HK domain 3, in this case amino acid residues Asn275-Lys282. The peptides inhibit endothelial cell proliferation and may also induce endothelial cell apoptosis. Compositions including the
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                                                                                                                                                                                                                                      Length 32;
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                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Domaine 3, bradykinin release activating peptide.
                                                                                                                                                                                                                                    100.0%; Score 60; DB 21;
100.0%; Pred. No. 0.00097;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR33350 standard; protein; 117 AA.
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Best Local Similarity 100.
Matches 12; Conservative
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                                                                                                                                                                                  32 AA;
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Composition for inhibiting angiogenesis and endothelial cell proliferation, inducing endothelial cell apoptosis and treating cancer, rheumatoid aryhritis, and ocular disorders comprises a kininogen domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kiningen (HK) The invention provides peptides (see AAY95405-24) that are analogues of certain sites in the HK domain 3. Specifically Ash275-Lys282, Cys246-Cys249, Leu331-Tyx38 and Tyr299-Ser314. The peptides, in which native Cys residues may be replaced by Ala residues, inhibit endothelial cell proliferation and may also Anduce endothelial cell apoptosis. Compositions including—The peptides are used in claimed methods for inhibiting endothelial cell proliferations and gomesis, inhibiting endothelial cell proliferation, and conjug endothelial cell apoptosis. Cancer, rheumatoid arthritis, and coular disorders characterized by undesired vascularization of
                                                                                                                                                                     Anti-anglogenic; anglogenesis; inhibitor; kininogen; homologue; endothelial cell proliferation; apoptosis; cancer; ocular disorder; rheumatoid arthritis; cytostatic; antiarthritic; antirheumatic; therapy; human; D3 peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 60; DB 21; Length 123; 100.0%; Pred. No. 0.0047; ive 0; Mismatches 0; Indels
                                                                                                                                     Human high mgl.wt. kininogen domain 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 4; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                       .98US-0112427.
                                                                                                                                                                                                                                                                                                                                                                     99WO-US28465.
                                                                                                 Wirst entry)
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(MCCR/) MCCRAE/R K.
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                                                                                                                                                                                                                                                                                                                                                                     02-DEC-1999;
                                                                                                 25-SEP-2000
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in secretion of endothelial cell contents such as tissue plasminogen activator and von Willebrand factor. Domain 3 functions to inhibit cell activation by blocking thrombin binding to its target cells, the peptide is a selective inhibitor of thrombin-induced platlet activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inhibition of mammalian legumain or legumain-related endopeptidase by cystatin involves interaction with second papain-non-reactive site of
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llarity 100.0%; Pred. No. 0.0046;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                               AAB37447 standard; protein; 122 AA.
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                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
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Best Local Similarity
Matches 12; Conserv
                                                                                                                117 AA;
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Novel human diagnostic protein #21093.

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food supplement; medical imaging; diagnostic; genetic disorder.
                            Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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100.0%; Pred. No. 0.011;
iive 0; Mismatches (
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                                                                                                                     30-MAR-2001; 2001WO-US08631.
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23-AUG-2000; 2000US-0649167.
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Matches 12; Conserv
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                                         Homo sapiens.
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags of the indefinity of the second in the
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                                                                                                                                                                                                                               30-MAR-2001; 2001WO-US08631.
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23-AUG-2000; 2000US-0649167.
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Matches 12; Conservative
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N-PSDB; AAS85286.
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WO200175067-A2.
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Homo sapiens.

11-0CT-2001

biodiversity

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The invention relates to isolated polynuclectide (1) and polypeptide (11) sequences. (1) is useful as hybridisation probes, polymerase frain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (1) is useful in gene therapy techniques to resome normal activity of (II) or to treat disease states involving (II). (IF) is useful for generating antibodies against it, detecting or quantifacting a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disolates linvolving abbrrant protein expression or biological activity. The polypebtide and polynucleotide sequences have applications in caponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human and as and to produce data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated/polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 60; DB 22; Length 644; 100.0%; Pred. No. 0.032;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'nt/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID No 51460; 103pp; English.
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380..388
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                                                                                                                                                                                                                                                                                                                 Tang YT;
                                                                                                                                           30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                         31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                              iu C,
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Best Local Similarity
Matches 12; Gonserva
                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-639862/73
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                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAS85288.
                                           WO200175067-A2
                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              at ftp.wipo.
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                                                                                           11-OCT-2001.
                                                                                                                                                                                                                                                                                                                 Drmanac RT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20;
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Peptide
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polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques or restore normal activity of (II) susful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical cinsorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic anino acid sequences. ABG00010-ABG30377 represent novel human caid sequence data for this patent id not appear in the printed specification, but was obtained in electronic format directly from WIPO control of the WIPO int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          n; chromosome mapping; gene mapping; gene therapy; forensic; supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 20; SEQ ID No 51464; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human diagnostic protein #21092.
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                                                                                                                                                                                                                                                                                                                                     Tang YT;
                                                                                                                                                                30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                              31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
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Best Local Similarity 100.
Matches 12; Conservative
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                                                                  WO200175067-A2
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Sequence

ABG21101;

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ABG21101 RESULT

Human;

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Gaps

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19-DEC-2001 (first entry)
                                                                                                                                                                                                                     Human neuroendocrine VGF.
                                                                                                Conservative
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                                                                        Query Match
Best Local Similarity
'-has 8; Conservē
                                                                                                                        | |:| |||||
279 InhsiakInae 289
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                                                                                                                2 LTHTITKLNAE 12
                                                         AA;
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                                                         434
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                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                     AAU09069;
                                                         Sequence
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                                                                                                                                                                    Bradykinin is a peptide consisting of nine amino acids. It has the biological effect of decreasing blood pressure. Although kininogen is known as a protein-precursor of bradykinin, its structure is unknown because of the difficulty in collecting large enough samples of kininogen for structural investigation.
                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                     c-Dna fragment of protein precursor - used to code bradykinin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3-Dng fragment of protein precursor - used to code bradykinin
        393..397
/note= "probe (AAN40241)-encoded sequence"
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/note= "probe (AAN40241)-encoded sequence"
                                                                                                                                                                                                                                           Length 436;
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                                                                                                                                                                                                                                                                                                                                                                                Bradykinin protein precursor: type II (pKG146, pKG254).
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                                                                                                                                                                                                                                           Score 42; DB :
Pred. No. 29;
2; Mismatches
                                                                                                                                                                                                                                           DB
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                                                                                                                                                                                                                                                                                                                                                                                                                        378..386
/label= bradykinin
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'label= bradykinin
                                                                                                                                                     Disclosure; Fig 2; 6 pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                Blood pressure; kininogen; probe..
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                                                                                               (MITU ) MITSUBISHI CHEM IND KK.
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                                                                                83JP-0000984.
                                                                                                                                                                                                                                          70.0%;
ilarity 72.7%;
Conservative
                                                                83JP-0000984
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                                                                                                              WPI; 1984-216122/35.
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281 lshsiaklnae 291
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                                                                                                                                                                                                                                                                          2 LTHTITKLNAE 12
                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                    436 AA;
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                                                                                                                       N-PSDB; AAN40242
                                JP59125896-A
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                                                                07-JAN-1983;
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                                                20-JUL-1984
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         Peptide
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Bradykinin is a peptide consisting of nine amino acids. It has the biological effect of decreasing blood pressure. Although kininogen is known as a protein-precursor of bradykinin, its structure is unknown because of the difficulty in collecting large enough samples of kininogen for structural investigation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     formulating a pharmaceutical preparation including one or more agents identified as having an acceptable therapeutic profile and/or licensing to a third party the rights for further drug development of the identified agents. The method of conducting drug discovery business further comprises an additional step of establishing a distribution
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                    Length 434;
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Pred. No. 43;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                               68.38;
72.78;
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system for distributing the preparation for sale and may optionally include establishing a sales group for marketing the preparation. A pharmaceutical composition containing the agent is useful for enhancing memory consolidation in an animal, or for augmenting learning and memory or otherwise for enhancing the functional performance of central nervous system neurons, where the agent is a cAMP elevating agent (agonist) preferably a cAMP analogue or CAMP phosphodiesterase inhibitor, which activates adenylate cyclase. The composition is useful for treating due to toxicant exposure, brain injury, epilepsy, mental retardation in children and senile dementia, including Alzheimer's disease. The present sequence represents human neuroendocrine VGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, namunomodulatory activity and activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; cytokine; cell proliferation; cell differentiation; gene therapy; vacchie; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
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                                                                                                                                                                                                                                                                                                         22; Length 616;
                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                       Score 41; DB 2
Pred. No. 64;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA012939 standard; Protein; 669 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human polypeptide SEQ ID NO 26831.
                                                                                                                                                                                                                                                                                                       68.3%;
58.3%;
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18-MAY-2000; 2000US-0577409.
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                                                                                                                                                                                                                                                                                                                                           7; Conservative
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| 187 trthtltrvnle 198
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Best Local Similarity
Matches 7; Conserv
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Composition for inhibiting angiogenesis and endothelial cell proliferation, inducing endothelial cell apoptosis and treating cancer, rheumatoid arthritis, and ocular disorders comprises a kininogen domain
                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is that of a D3 peptide derived from human high mol.wt. Kiningen (HK) domain 3 (see AAY59426). The D3 peptide inhibits endothelial cell proliferation and thus possesses anti-anglogenic activity. It is an example of D3 peptides of the invention (see AAY95405-26) that are analogues of certain sites in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the HK domain 3, in this case amino acid residues Ash275-Lys282. The peptides inhibit endothelial cell proliferations and may also induce endothelial cell apoptosis. Compositions including the peptides are used in claimed methods for inhibiting angiogenesis, inhibiting endothelial cell proliferation, and inducing endothelial cell apoptosis. Cancer, rheumatoid arthitis, and coular disorders characterized by undesired vascularization of the retina are treated inhibition of fibroblast growth factor-induced HVVEC cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-anglogenic; anglogenesis; inhibitor; kininogen; homologue; endothelial cell proliferation; apoptosis; cancer; ocular disorder; rheumatoid arthritis; cytostatic; antiarthritic; antirheumatic; therapy; human; D3 peptide.
                                                                                                                                                                                ö
                                                                                                                                                 Length 669;
                                                                                                                                                                              2; Indels
                                                                                                                                             Score 41; DB 22;
Pred. No. 71;
3; Mismatches 2
                                                                                                                                                                                                                                                                                                                              AAY95409 standard; Peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 6; Page 26; 44pp; English.
                                                                                                                                             68.3%;
58.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-angiogenic D3 peptide.
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                                                                                                                                                                                  7; Conservative
                                                                                                                                                                                                                                  1 TLTHTITKLNAE 12
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                                                                                                                                               Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                               669 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-DEC-1998;
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                                                                                                  Seguence
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                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Human; pancreas; pancreatic cancer; pancreatic cancer antigen; detection; diagnosis; identification; cytostatic; neuroprotective; nootropic; immunomdulatory; relaxant; contraceptive; gynaecological; antlinflammatory; cardiant; gene therapy; chromosome mapping; linkage analysis; tissue identification; tissue typing; forensic; neural; immune system; muscular; reproductive; gastrointestinal; pulmonary; cardiovascular; renal; proliferative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid that is a pancreatic cancer antigen for preventing, treating, or ameliorating a medical condition, particular pancreatic cancer, or for use in assays for diagnosing a pathological condition
                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC98773 to AAC99231 encode the human pancreatic cancer associated
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                                                    Score 38; DB 21; Length 16; Pred. No. 3.1;
                                                                                              0; Indels
                                          63.3%; Scor.
100.0%; Pred. No. ...
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                                                                                                                                                                                                                                                                    AAB54127 standard; Protein; 210 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0124270.
                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                8; Conservative
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N-PSDB; AAC98892.
                                                        Query Match
Best Local Similarity
  16 AA
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                                                                                                                                                                                                                                                                                                          AAB54127;
  Sequence
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                                                                                              Matches
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CC proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent
CC sequences used in the exemplification of the present invention.
XX
SQ Sequence 210 AA;
SQ Sequence 210 AA;

Query Match
Best Local Similarity 58.3%; Score 38; DB 21; Length 210;
Best Local Similarity 58.3%; Pred. No. 61;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy 1 TLTHTITKLNAE 12
|||| :|||
Db 183 tlthyvrpinae 194
Search completed: July 1, 2002, 16:19:43
Job time: 147 sec
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114, 115, 113, 112,

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Sequence Sequence

Sequence Sequence

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GENERAL INFORMATION:
APPLICANT: Schmaler, Alvin H.
APPLICANT: Schmaler, Alvin H.
APPLICANT: Jiang, Yongping
TITLE OF INVENTION: Midulation of Blood
TITLE OF INVENTION: With Kininogen Fragment
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schdel, Gonda, Lavorgna &
ADDRESSEE: Monghoo, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CUCREENT APPLICATION DATA:
APPLICATION NOMBER: US/08/193,114B
FILING DATE: (9 February 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Application
APPLICATION NUMBER: Serial No. 5472945 07/744,545
FILING DATE: /13 August 1991
ATTORNEY/AGENT ANDORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 60; DB 1; 1
Pred. No. 0.00095;
                            US-09-198-723A-14
US-09-198-723A-15
US-09-198-723A-15
US-09-198-723A-16
US-09-198-723A-18
US-09-198-723A-19
US-09-198-723A-20
US-08-867-941-20
US-08-867-941-17
US-08-867-941-17
US-09-074-658-13
US-09-074-658-13
                                                                                                                                                                                                                                                 US-08-867-941-12
US-08-867-941-16
US-09-074-658-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Monago, Daniel A.
REGISTRATION NUMBER: 30,480
REPERENCE DOCKET NUMBER: 6056-137 CII
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-549
TELEEX: NO. 3472945e
INFORMATION FOR $EQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: / Diskette, 3.50 inch, 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Monaco, P.C.
STREET: 1800 Two Penn Center Plaza
CITY: Philadelphia
STATE: Pennsylvania
CUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                          US-08-193-114B-1
; Sequence 1, Application US/08193114B
; Patent No. 5472945
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OPERATING SYSTEM: MS-DOS
SOFTWARE: WOXGPERFECT 5.1
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LENGTH: 117
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                                                                                                           July 1, 2002, 16:18:00 ; Search time 35.15 Seconds (without alignments) 8.339 Million cell updates/sec
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Sequence 46,
Sequence 44,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence 44, sequence 44, sequence 44, sequence 7, sequence 7, sequence 7, sequence 21, sequence 1, sequence 1, sequence 2, sequence 2, sequence 23, sequence 25, sequence 25, sequence 25, sequence 60,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 46,
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Sequence 7
Sequence 7
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- 2000 Compugen Ltd
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PCT-US92-06809-1
US-08-483-695-46
US-08-487-231-46
US-08-201-912-46
US-08-134-917-44
US-08-134-616-44
US-08-134-616-44
US-08-134-65-44
US-08-135-685-7
US-08-135-85-7
US-08-135-85-7
US-08-135-135-13
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Maximum Match 100%
Listing first 45 summaries
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                 GenCore
Copyright (c) 1993
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                                                                                                                                                                                                                   Sednence:
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Result No.

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APPLICANT: Brechot, Christian
APPLICANT: Brechot, Chia
APPLICANT: Kremadorf Colette
APPLICANT: Porchon, Colette
TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic
TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                         ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,695
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/965,285
FILING DATE: 18-WAR-1993
APLING DATE: 18-WAR-1993
ATORNEY/AGENT INFORMATION:
NAME: MAYORS, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENE/POCKET NUMBER: 05286-0001-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 35; DB 2;
Pred. No. 42;
0; Mismatches 1
                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 46, Application US/07965285 Patent No. 5879904 GENERAL INFORMATION:
  TITLE OF INVENTION: Applications
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ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-D
                                                                                              STREET: 1300 I Street, N.W. CITY: Washington
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87.5%;
                                                                                                                                                                                                                            Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 189 amino acids
amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                               ZIP: Z0005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) MOLECULE TYPE: peptide US-08-483-695-46
                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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182 TLTHPITK 189
                                                                                                                                                                  USA
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                                                                                                                                                                  COUNTRY:
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US-08-483-695-46
Sequence 46, Application US/08483695
Sequence 46, Application US/08483695
Patent No. 5866139
GENERAL INFORMATION:
APPLICANT: Brechot, Christian
APPLICANT: Kremsdorf, Dina
APPLICANT: Porchon, Colette
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a
TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic
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                                                                                                                                                                          Sequence 1, Application PC/TUS9206809
GENERAL INFORMATION:
APPLICANT: Schmaier, Alvin H.
APPLICANT: Jiaqy, Yongping
TITLE OF INVENTION: Modulation of Blood
TITLE OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 60; DB 5; Length 117; 100.0%; Pred. No. 0.00095;
0; Indels
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                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Temple University - Of the
ADDRESSEE: Temple University - Of the
STREET: Commonwealth System of Higher Education
STREET: Building
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
COMPUTER: IEM PS/2
COMPUTER: IEM PS/2
COMPUTER: IEM PS/2
COMPUTER: IEM PS/2
COMPUTER: WordPerfect 5.1
CURRENT MOTABLE: 19910813
CLASSIFTCATION DATA:
APPLICATION NUMBER: PCT/US92/06809
FILING DATE: 19910813
CLASSIFTCATION S14
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Application
APPLICATION NUMBER: Serial No. 744,545
FILING DATE: 13 ANGUST 1991
ATTORNEY AGENT INFORMATION:
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REGISTRATION NUMBER: 6056-137
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 117 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12; Conservative
                                                           18 TLTHTITKLNAE 29
                                      1 TLTHTITKLNAE 12
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Best Local Similarity
Matches 12; Conserva
                                                                                                                                          RESULT 2
PCT-US92-06809-1
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Matches
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Sequence 46, Application US/09201912

Sequence 46, Application US/09201912

Patent No. 6210962

GENERAL INFORMATION:
APPLICANT:
APPLICANT:
Forchon, Colette
TITLE OF INVENTION:
NUCLE-COLOR INFORMATION:
NUCLE-COLOR INFORMATION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET:
STREET:
ADDRESSEE: NUMBER OF SECURATION:
ADDRESSEE: Dunner
STREET:
ADDRESSEE: NUMBER OF SECURATION:
ADDRESSEE: NUM
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 189; 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 35; DB 4; Length 189;
Pred. No. 42;
0; Mismatches 1; Indels
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ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-POS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05286-0001-00000
                                                                                                                                                                                                                                                                                                                                                                           Score 35; DB Pred. No. 42; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/201,912
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CLASSIECATION
PRICA APPLICATION
APPLICATION NUMBER: 07/965,285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25,146
                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Meyers, Kenneth J. REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 05,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                      TELEPHONE: 202-408-4000

TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 44, SEQUENCE CHARACTERISTICS: LENGTH: 189 amino acids: TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: peptide US-08-487-231-46
                                                                                                                                                                                                                                                                                                                                                                              58.38;
87.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 87.37
Conservative 7;
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity 87.5
Matches 7; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide US-09-201-912-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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182 TLTHPITK 189
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USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TLTHTITK 8
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US-09-201-912-46
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                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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APPLICANT: Kremsdorf, Dina
APPLICANT: Kremsdorf, Dina
APPLICANT: Forthon, Colette
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a
TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic
TITLE OF INVENTION: Applications
WIMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Pred. No. 42;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC COMPATIBLE FORM:
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPANION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,231
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/965,285
FILING DATE: 18-MAR-1993
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION NUMBER: FR 91 06 882
FILING DATE: 06-JUN-1991
ATPORNEY/AGENT INFORMATION:
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/965,285
                                                                                                                                  PRIOR APPLICATION: 435

PRIOR APPLICATION DATA: APPLICATION NUMBER: FR 91 06 882

FILING DATE: 06-JUN-1991

ATTORNEY-AGENT INFORMATION: NAME: MAWE: MAWE: MAWE: AFFATION NUMBER: 25,146

REFERENCE/DOCKET NUMBER: 05286-0001-00000

TELECOMMUNICATION INFORMATION: TELEPHONE: 202-408-4400

TELEPHONE: 202-408-4400

INFORMATION FOR SEQ ID NO: 46: SEQUENCE CHARACTERISTICS: LENGTH: 189 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 05286-0001-02000
                                                         UMBER: US/07/965,285
18-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 46, Application US/08487231
Patent No. 5919454
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 58.3%;
Best Local Similarity 87.5%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 189 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: peptide US-07-965-285-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20005-3315
COMPUTER READABLE FORM:
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ZIP: 20005-3315
                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||||| |||
182 TLTHPITK 189
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US-08-487-231-46
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Gaps
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APPLICANT: OKAYAMA, Hiroto
APPLICANT: FUKE, ISAO
APPLICANT: MORI, Chisato
APPLICANT: MORILA, Chisato
APPLICANT: YOSHIDA, IWAO
TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
TITLE OF INVENTION: ONN-A, NON-B HEPATITIS VIRUS GENOMIC
TITLE OF INVENTION: ONN-A, NON-B HEPATITIS VIRUS GENOMIC
TITLE OF INVENTION: WAS AND ANTIGEN POLYPEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Armstrong, Westerman, Hattori, McLeland &
ADDRESSEE: Naughton
STREET: 1725 K St. N.W. Suite 1000
STREET: D.C.
STREET: D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CALF: 2000
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/384,616
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/384,616
FILING DATE: 0.00T-1991
APPLICATION NUMBER: US 07/769,996
FILING DATE: 25-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-167466
FILING DATE: 31-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/635,451
FILING DATE: 28-DEC-1990
APPLICATION NUMBER: SEDEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: SELENGENEY/AGENT INFORMATION:
NAME: SELENGENEY/DOCKET NUMBER: 36,281
RESTRENCE/DOCKET NUMBER: 36,281
REFERENCE/DOCKET NUMBER: 36,281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                          RESULT 8
US-08-384-616-44
; Sequence 44, Application US/08384616
; Septent No. 5847101
; GENERAL INFORMATION:
; APPLICANT: OKAYAMA, Hiroto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2930
TELEFAX: (202) 887-0357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 58.3%;
Best Local Similarity 87.5%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RY: U.S.A.
20006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1111 |||
21 TLTHPITK 28
                                          21 TLTHPITK 28
  1 TLTHTITK 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-384-616-44
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                                                                                                                                                                                                                                           APPLICANT: FUKE, ISAO
APPLICANT: MORI, Chisato
APPLICANT: TAKAMIZAWA, Akahisa
APPLICANT: TAKAMIZAWA, Akahisa
APPLICANT: YOSHIDA, IWAO
TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Armstrong, Westerman, Hattori, McLeland & ADDRESSEE: Naughton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PATOL AFTLICALION DATA:
PRELICATION NUMBER: 19 2-230921
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 32 -305605
FILING DATE: 09-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/099,706
FILING DATE: 30-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/769,996
FILING DATE: 02-OCT-1991
PRIOR APPLICATION NUMBER: US 07/635,451
FILING DATE: 28-DEC-1990
ATTORNEY/AGENT INFORMATION:
RAME: Stevens-Smith, Theresa M.
REGISTRATION NUMBER: 86,281
REGISTRATION NUMBER: 900703D
TELEPHONE: (202) 659-2330
TELEPRAS: (202) 659-2330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1725 K St. N.W. Suite 1000 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/324,977
FILING DATE: 18-OCT-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: JP 2-167466
FILING DATE: 25-JUN-1990
PRIOR APPLICATION DATA:
                                                                                                                                                    Sequence 44, Application US/08324977
Patent No. 5747339
GENERAL INFORMATION:
APPLICANT: OKAYAMA, Hiroto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 440142
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                      OKAYAMA, Hiroto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 247 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein US-08-324-977-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRY: U.S.A.
20006
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182 TLTHPITK 189
1 TLTHTITK 8
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                                                                                                                                 US-08-324-977-44
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TELEX: 4
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21 TLTHPITK 2

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APPLICANT: OKAYAMA, HITOTO
APPLICANT: FUKE Isao
APPLICANT: MORI, Chisato
APPLICANT: TAKAMIZAWA, Akahisa
APPLICANT: YOSHIDA, Iwao
TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
                                                                                                                                                                                                                                                                                                                                                  mstrong, Westerman, Hattori, McLeland &
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                                                                                                                                                                                                                                                                                                                                                                                             .K St. N.W. Suite 1000
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APPLICATION NUMBER: US/08/904,686
FILING DATE: 01-AUG-1997
APPLICATION NUMBER: US 08/324,977
FILING DATE: 18-CCT 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 2-167466
FILING DATE: 25 JUN 1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 2-230921
FILING DATE: 31 AUG-1990
PRIOR APPLICATION NUMBER: UP 2-305605
FILING DATE: 05-KOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER: US/08/904,686
01-AUG-1997
NUMBER: US 08/324,977
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APPLICATION DAMBER: US 07/769,996
FILING DATE:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATION DATA:
NUMBER: US/09/315,850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/635,451
                                                                                    Sequence 44, Application US/09315850 Patent No. 6217872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE MA DATE: 28 -DEC-1990
ATTORNEY-AGENT INFORMATION:
NAME: MCDeland, Le-Nhung
REGISTATION NUMBER: 31,541
REFERENCE/DOCKEY NUMBER: 9007
TELECOMMUNICATION NUMBER: 9007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (202) 659-29:
TELEFAX: (202) 887-0357
INFORMATION FOR SEG ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 30-JUL-1
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                 GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                STREET: 1745 CITY: Washing STATE: D.C.
                                                                                                                                                                                                                                                                                                     NUMBER OF SECUEN
CORRESPONDENCE A
ADDRESSEE: AT
ADDRESSEE: NA
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                                                                 US-09-315-850-44
                                  Sequence 44, Application US/08904686A

Patent No. 5993130

GENERAL INFORMATION:
APPLICANT: CKAYAMA, Hiroto
APPLICANT: FUKE, Isao
APPLICANT: TARAMIZAWA, Akahisa
APPLICANT: TARAMIZAWA, Akahisa
APPLICANT: TOSHIDA, Ivao
TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
NUMBER OF SEQUENCES: 50
CORRESSEDE: Armatrong, Westerman, Hattori, McLeland & ADDRESSEE:
ADDRESSEE: Anaughton
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRICHICATION NUMBER: JP 2-230921
FILING DATE: 31-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-305605
FILING DATE: 09-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/099,706
FILING DATE: 30-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/324,977
FILING DATE: 18-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-167466
FILING DATE: 25-UN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-230921
                                                                                                                                                                                                                                                                                                                                                1725 K St. N.W. Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/904,686A
FILING DATE: 01-AUG-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/769,996
FILING DATE: 02-0CT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/635,451
FILING DATE: 28-DEC-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: McLeland, Le-Nhung
REGISTRATION NUMBER: 31,541
REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (202) 659-2930
TELEFAX: (202) 887-0357
INFORMATION FOR SEQ ID NO: 44:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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U.S.A.
                                                                                                                                                                                                                                                                                                                                                                    Washington
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RESULT 9
US-08-904-686A-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-904-686A-44
                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                    CITY: W
STATE:
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58)3%; Score 35; DB 4; Length 247;

Query Match

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Score 35; DB 2; Length 247; Pred. No. 57; 0; Mismatches 1; Indels

) MOLECULE TYPE: protein US-09-315-850-44

Query Match 58.3%; Best Local Similarity 87.5%; Matches 7; Conservative

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GENERAL INFORMATION:
APPLICANT: Brechot, Christian
APPLICANT: Brechot, Colette
APPLICANT: Remedorf Colette
TITLE OF INVENTION: Nuclectide and Peptide Sequences of a
TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic
TITLE OF INVENTION: Applications
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
STRET: 1300 I Street, N.W.
CITY: Washington
STATE: DC
                                         TITLE OF INVENTION: Nucleotide and Peptide Sequences of a TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic TITLE OF INVENTION: Applications NUMBER OF SEQUENCES: 46
                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/965,285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 35; DB 2;
Pred. No. 73;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05286-0001-00000
                                                                                                                                                                                                                                                                                                                                                                                               PAPLICATION NUMBER: US/07/965,285
FILING DATE: 18-MAR-1993
CLASSIEFCATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION NATA:
APPLICATION NUMBER: FR 91 06 882
FILING DATE: 06-UNF-1991
ATTONNEY, AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERNCE/DOCKET NUMBER: 05286-0001-TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/08487231 Patent No. 5919454
                                                                                                                                                                                     1300 I Street, N.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 313 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: peptide US-07-965-285-7
                                                                                                                                                                                                        Washington
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Best Local Similarity
Matches 7; Conserv
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ZIP: 20005-3315
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182 TLTHPITK 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                            STATE:
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                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Brechot, Christian
APPLICANT: Kremsdorf, Dina
APPLICANT: Porchon, Colette
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a
TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic
TITLE OF INVENTION: Applications
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
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                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISON COMPATIBLE
OPERATING SYSTEM: PC.DOMSANS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/483,695
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 35; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 25,146
REFERENCE/ZDCXET NUMBER: 05286-0001-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
    Pred. No. 57;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 73;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION UNDER: US/07/965,285
FILING DATE: 18 MAR-1933
APPLICATION NUMBER: FR 91 06 882
FILING DATE: 06-UN-1991
ATTOM DATE: NEWATION:
NAME: MEYERS, KENNELLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
US-07-965-285-7
Sequence 7, Application US/07965285
Patent No. 5879904
GENERALINFORMATION:
APPLICANT: Brechot, Christian
                                                                                                                                                                                                     Sequence 7, Application US/08483695 Patent No. 5866139
                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1300 I Street, N.W.
87.5%;
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87.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acids
TYPE: amino acid
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Best Local Similarity 87.50
                         7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: peptide US-08-483-695-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |||| |||
182 TLTHPITK 189
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                                                                                     |||| |||
21 TLTHPITK 28
                                                              1 TLTHTITK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
STREET: 13
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US-08-483-695-7
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Length 313;

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APPLICANT: Du, Run-Pan
APPLICANT: Wang, Quijun
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
NUMBER OF SEQUENCES: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

S8.3%; Score 35; DB 4; Length 313;
Best Local Similarity 87.5%; Pred. No. 73;
Matches 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 58.3%; Score 35; DB 2; Length 585; Best Local Similarity 87.5%; Pred. No. 1.5e+02; Matches 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M52 IR7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM FC Componatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.3(
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,941
FILING DATE: 03-JUN-1997
CLASSIPTCATION: WIMBER: 24,973
REFERENCE/DOCKET UNMBER: 24,973
REFERENCE/DOCKET UNMBER: 24,973
REFERENCE/DOCKET UNMBER: 1038-681 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1165
TELEPHONE: (416) 595-1163
SEQUENCE CHARACTERISTICS:
LENGTH: S85 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Version #1.30
   25,146
FR: 05286-0001-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-867-941-21
; Sequence 21, Application US/08867941
; Patent No. 5977337
; GENERAL INFORMATION:
      REGISTRATION NUMBER: 25,146
REPERENCE/DOCKET NUMBER: 05.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
                                                                                                                                      TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                          LENGTH: 313 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-201-912-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |||| |||
182 TLTHPITK 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TLTHTITK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TLTHTITK 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Brechot, Christian
APPLICANT: Kremsdorf, Dina
APPLICANT: Kremsdorf, Dina
APPLICANT: Kremsdorf, Dina
APPLICANT: Kremsdorf, Colette
APPLICANT: Nucleotide and Peptide Sequences of a
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a
TITLE OF INVENTION: Applications
APPRESSE: Finnegan, Applications
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
CITY: Maghington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
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                                                   CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/487,231

FILING DATE: 07-JUNE-1995

CLASSIFICATION DATA:

APPLICATION NUMBER: US/08/5,285

FILING APPLICATION DATA:

APPLICATION NUMBER: US 07/965,285

FILING DATE: 18-MAR-1993

CLASSIFICATION APPRICATION DATA:

APPLICATION NUMBER: FR 91 06 882

FILING DATE: 18-MAR-1991

ATTORNEY AGENT INFORMATION:

NAME: Meyers, Kenneth J.

REGISTRATION NUMBER: 25,146

REFERENCE/DOCKET NUMBER: 05286-0001-02000

TELECOMMUNICATION INFORMATION:

TELEPAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 313 annino acids

TYPE: annino acids

TYPE: ANDINO acids

TELEPAX: ACIDS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-CONSTANT PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/201,912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 35; DB 2;
Pred. No. 73;
0; Mismatches
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/965,285
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/09201912
Patent No. 6210962
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 58.3%;
Best Local Similarity 87.5%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Meyers, Kenneth J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-487-231-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |||| |||
182 TLTHPITK 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
US-09-201-912-7
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Db 510 TLTHTIPK 517

Search completed: July 1, 2002, 16:18:00 Job time: 44 sec

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Sequence 3 Sequence 4 Patent No.

Sequence

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APPLICANT: Schmaier, Alvin H.
APPLICANT: Jiang, Yongping
TITLE OF INVENTION: Modulation of Blood
TITLE OF INVENTION: Pressure and Inhibition of Platelet Activation
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/193,114B
FILING DATE: 9 February 1994
CLASSIFICATION S14
PRIOR APPLICATION NUMBER: U.S. Application
APPLICATION NUMBER: Serial No. 5472945 07/744,545
FILING DATE: 13 August 1991
ATTORNEY/AGENT INFORMATION:
NAME: MONGCO. DARIO.
US-08-446-100-6
US-08-446-100-6
US-08-446-100-9
US-08-446-100-9
US-08-446-100-10
US-08-446-100-13
US-08-446-100-13
US-08-446-100-13
US-08-446-100-14
US-08-446-100-15
US-08-446-100-16
US-08-446-100-16
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US-08-446-100-17
US-08-446-100-18
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US-08-446-100-18
US-08-446-100-18
US-08-446-100-18
                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Seidel, Gonda, Lavorgha ADDRESSEE: Monaco, P.C. CYREET: 1800 Two Penn Center Plada CITY: Philadelphia
                                                                                                                                                                                                              5215909-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6056-137
                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08193114B Patent No. 5472945
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
TELEFAX: No. 54729456
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide
   TOPOLOGY:
                                                                                                                                                                                                                                                                                               US-08-193-114B-1
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  Sequence 1, Appli
Sequence 15, Appli
Sequence 30, Appl
Sequence 36, Appl
Sequence 8, Appli
Sequence 8, Appli
Sequence 9, Appli
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Appli
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Patent No. 5200183
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                                                                                                  (without alignments)
5.559 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence 8, A
Sequence 8, A
Sequence 8, A
Sequence 8, A
Sequence 8, A
Sequence 9, A
Sequence 28, A
Sequence 28, A
Sequence 6, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
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                                                                                   July 1, 2002, 16:17:16 ; Search time 35.15 Seconds
                                                                                                                                                                                                                                                                                                                                                                      /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
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/cgn2_6/ptodata/2/iaa/pcTuCS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/pcTuCS_COMB.pep:*
            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-676-242-15
US-08-483-140-30
US-08-483-140-30
US-08-318-905-8
US-08-483-123-8
US-08-483-140-8
US-09-328-474-8
US-09-100-546-8
US-08-483-140-28
US-08-480-604A-6
US-08-480-604A-6
US-08-480-604A-6
US-08-480-604A-6
US-08-915-136-6
                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-446-100-2
US-08-446-100-3
US-08-446-100-4
                                                                                                                                                                                                                        231628 seqs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                            - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5200183-5
                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                            Issued_Patents_AA:*
                                                                                                                                                                                                                                                                        seq length: 0 seq length: 2000000000
                                                                                                                                   US-09-461-061A-1
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                                                                                                                                                            1 NNATFYFK 8
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Match Length
                                                                                                                                                 Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                       Minimum DB
Maximum DB
                                                            OM protein
                                                                                                                                                              Sequence:
                                                                                                                                                                                                                        Searched:
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                                                                                     Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Result
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720

Length 117;

DB 1;

CII

0.16;

45; No.

Gaps

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Length 26;

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OTHER INFORMATION: Description of Artificial Sequence: Bradykinin; OTHER INFORMATION: analog
US-08-676-242-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gertein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 30, Application US/08483140
Patent No. 5598403
GENERAL INFORMATION:
APPLICANT: ICOS Corporation
TITLE OF INVENTION: Platelet-Activating Factor Acetyl
TITLE OF INVENTION: Hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,140
                                                                                                                                                                                                                                                                                                                                                                                                         86.7%; Score 39; DB 4; 100.0%; Pred. No. 0.43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
CURRENT APPLICATION NUMBER: US/08/676,242C CURRENT FILING DATE: 2000-07-16
EARLIER APPLICATION NUMBER: 60/000,096
EARLIER FILING DATE: 1995-06-09
EARLIER TILING DATE: 1995-06-07
EARLIER FILING DATE: 1996-06-07
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 6-0CT-1994
PRIOR APPLICATION NUMBER: US 08/133,803
FILING DATE: 6-0CT-1993
ATTOCNEY/AGENT INFORMATION:
NAME: NO. 5698403and, Greta E.
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 32781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 193 amino acids
amino acid
3Y: linear
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.(
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 60606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 NATFYFK 8
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                                                                                                                                                                                  SEQ ID NO 15
LENGTH: 26
                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                                                            FEATURE:
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Sequence 15, Application US/08676242C
Battent No. 6143719
GENERAL INFORMATION:
APPLICANT: The Regents of the University of Michigan
APPLICANT: Schmaier, Alvin H.
APPLICANT: Hasan, Ahmed A.K.
TITLE OF INVENTION: Bradykinin Analogs As Selective Thrombin Inhibitors
FILE REFERENCE:* 8820-2 US
         Gaps
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                                                                                                                                                                                                                                            APPLICANT: Schmeler, Alvin H.
APPLICANT: Schmeler, Alvin H.
APPLICANT: Jiang, Yongping
TITLE OF INVENTION: Modulation of Blood
TITLE OF INVENTION: Pressure by Altering Bradykinin Levels
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Temple University - Of the
ADDRESSEE: Commonwealth System of Higher Education
STREET: 406 University Services
STREET: Bullding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 45; DB 5; Length 117; 100.0%; Pred. No. 0.16;
         0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US92/06809
FILING DATE: 19910813
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Application
APPLICATION NUMBER: Serial No. 744,545
FILING DATE: 13 August 1991
ATORNEY/AGRNT INFORMATION:
NAME: MORACO, Daniel A.
REFERENCE/DOCKET NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-137
TELEPHONE: (215) 568-8383
TELEPHONE: (215) 568-8383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORDPERfect 5.1
CURRENT APPLICATION DATA:
         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                           RESULT 2
PCT-US92-06809-1
PCT-US92-06809-1, Application PC/TUS9206809
GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 8; Conservative
    8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Building
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear PCT-US92-06809-1
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                                                1 NNATFYFK 8
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US-08-676-242-15
      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Marshall, O'Toole, Gertein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                         GENERAL INFORMATION:
APPLICANT: COUSENS, LAWRENCE S.
APPLICANT: Gray, Patrick W.
APPLICANT: Tjoelker, Larry W.
APPLICANT: Tjoelker, Larry W.
APPLICANT: Tjoelker, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor Acetyl
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Gray, Patrick W.
APPLICANT: Le Trong, Hai
APPLICANT: Lie Trong, Hai
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor Acetyl
TITLE OF INVENTION: Hydrolase
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: 0300 Sears lower, 233 South Wacker Drive CITY: 0500 Sears lower, 233 South Wacker Drive STATE: 11linois COUNTRY: USA ZIP: 06060 COMPUTER READABLE FORM: WEDLUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/470,187 FILING DATE: CLASSIFICATION DATA: APPLICATION NUMBER: APPLICATION NUMBER: OF THE CLASSIFICATION DATA: APPLICATION NUMBER: APPLICATION N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68.9%; Score 31; DB 1; 71.4%; Pred. No. 2e+02; ive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: NO. 552152and, Greta E.
REGISTRATION NUMBER: 35,302
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-318-905-8
Sequence 8, Application US/08318905
Patent No. 5641669
GENERAL INFORMATION:
APPLICANT: Cousens, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
                                   Sequence 8, Application US/08470187
Patent No. 5532152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-6448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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; MOLECULE TYPE: protein
US-08-470-187-8
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Best Local Similarity
Las 5; Conserva
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185 SATYYFK 191
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                                Score 31; DB 1; Length 193;
Pred. No. 89;
2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Illinois
COUNTRY: United States of America
ZUP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,938A
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cousens, Lawrence S.
APPLICANT: Cousens, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Tory, Patrick W.
APPLICANT: Torker, Larry W.
APPLICANT: Tjoeker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Placelet-Activating Factor
TITLE OF INVENTION: Acetylhydrolase
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 27866/32792
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-007-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-007-1993
ATTORNEY AGENT INFORMATION:
NAME: No. 5847088and, Greta E.
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                    Sequence 36, Application US/08485938A Patent No. 5847088 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 36:
                                68.9%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 amino acids amino acids
Query Match
Best Local Similarity /1...
Best Local Similarity /1...
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Best Local Similarity 71.4
Matches 5; Conservative
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LENGTH: 193 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chicago
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143 SATYYFK 149
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143 SATYYFK 149
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                                                                                                                                                                                                                                                                                                             RESULT 5
US-08-485-938A-36
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Gaps

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Length 441;
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STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: ICOS COrporation
TITLE OF INVENTION: Platelet-Activating Factor Acetyl
TITLE OF INVENTION: Hydrolase
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 31; DB 1;
Pred. No. 2e+02;
2; Mismatches
                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-0CT-1994
PRIOR APPLICATION DATE: 06-0CT-1994
FILING DATE: 06-0CT-1993
APPLICATION NUMBER: US 08/133,803
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5656431and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 37866/32689
TELECOMUNICATION INFORMATION:
TELECHONE: (312),474,6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 6-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 6-0CT-1993
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5698403and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32781
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-483-140-8
Sequence 8, Application US/08483140
; Patent No. 5698403
                                                                                                                                                                                                                                                                                                                                                               : LELERAX: (312) 474-6300
TELERAX: (312) 474-6448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino and TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68.98;
71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (312) 474-6300
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TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 68.9
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-08-483-232-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 6300 Sear
CITY: Chicago
STATE: Illinois
COUNTRY: USA
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185 SATYYFK 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 NATFYFK 8
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STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
ADDRESSEE: Marshall, O'Toole, Gertein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
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Sequence 8, Application US/08483232
Sequence 8, Application US/08483232
Sequence 8, Application US/08483232
Sequence 8, Applicant Cousens, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Eberhardt, Christine D.
APPLICANT: If Tioelker, Larry W.
APPLICANT: If Tioelker, Larry W.
APPLICANT: Wilder, Cherry L.
TITLE OF INVENTION: Platelet-Activating Factor
TITLE OF INVENTION: Acetylhydrolase
NUMBER OF SEQUENCES: 30
SEQUENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRE
                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,905
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APPLICATION NUMBER: US/08/483,232 FILING DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIPICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 6-0CT-1993
ATTONREY/AGENT INFORMATION:
NAME: NO. 5641669and, Greta E.
REGIENRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 3205
TELECOMMUNICATION INFORMATION:
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COUNTRY: United States of America
ZIP: 60606-6402
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-6448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Conservative
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Best Local Similarity
Matches 5; Conserva
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                                                                Chicago
Illinois
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185 SATYYFK 191
                                                                                                                                        USA
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                                                                                                                                    COUNTRY:
                                                                    CITY: C
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                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,041
                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Platelet-Activating Factor TITLE OF INVENTION: Acetylhydrolase NUMBER OF SEQUENCES: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 31; DB 2;
Pred. No. 2e+02;
2; Mismatches
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CLASSIFICATION: 424
PRIOR PAPLICATION DATA:
APPLICATION NUMBER: US 08/483,232
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
PRIOR APPLICATION NUMBER: US 08/133,803
APTICATION NUMBER: US 08/133,803
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: United States of America 2IP: 60606-6402
                                                                                                                                                                                                                             APPLICANT: Cousens, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: Larrong, Hai
APPLICANT: Tjoelker, Larry W.
APPLICANT: Tjoelker, Cheryl L.
                                                                                                                               RESULT 11
US-08-910-041-8
; Sequence 8, Application US/08910041
; Patent No. 5977308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 27 (ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEEX: 25-3658
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68.9%;
ilarity 71.4%;
Conservative
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Cousen
                                                      :||:|||
185 SATYYFK 191
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185 SATYYFK 191
                                 2 NATFYFK 8
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US-09-328-474-8
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Pred. No. 2e+02;
2; Mismatches 0; Indels
                                                                                                                                                                       Score 31; DB 1; Length 441; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Marshall, O'Toole, Gerstein, Murray & Borun
6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Cousens, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: Le Trong, Hai
APPLICANT: Tjoeker, Larry W.
APPLICANT: Wilder, Larry W.
TTLE OF INVENTION: Platelet-Activating Factor
TITLE OF INVENTION: Acetylhydrolase
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,938A
                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 35,302
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/32792
TELECOMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-6448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/318,905
FILING DATE: 06-OCT-1994
PRIOR APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Illinois
COUNTRY: United States of America
21P: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/08485938A Patent No. 5847088 GENERAL INFORMATION: APPLICANT: COUSENS, LAWRENCE S. APPLICANT: Eberhardt, Christine D.
                                                                                                                                                                     68.9%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
TOPOLOGY: 11-2
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Best Local Similarity 71.4%;
Matches 5; Conservative
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                                                                                                                                                                     Query Match 68.9
Best Local Similarity 71.4
Matches 5; Conservative
            SEQUENCE CHARACTERISTICS
                                                                                   ; MOLECULE TYPE: protein US-08-483-140-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-08-485-938A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 6300 & CITY: Chicago
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185 SATYYFK 191
                                                                                                                                                                                                                                                  2 NATFYFK 8
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GENERAL INFORMATION:

APPLICANT: Cousens, Lawrence S.
APPLICANT: Cousens, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Tjoelker, Larry W.
TTLE OF INVENTION: Platiet-Activating Factor
TITLE OF INVENTION: Acetylhydrolase
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 31; DB 3; Length 441; Pred. No. 2e+02;
                                                                         NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                            STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago
STATE: 111inois
STATE: 111inois
ZUNTRY: United States of America
ZIP: 60606-6402
COMPUTER: EDAPHE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,546
FILING DATE:
       APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor
TITLE OF INVENTION: Acetylhydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: NO. 609036and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/32793
TELEPONONE: (312) 474-6300
TELEPONE: (312) 474-630
TELEPAR: (312) 474-648
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
APPLICATION WUMBER:
FILING DATE:
FOR APPLICATION WUMBER:
APPLICATION WUMBER:
APPLICATION WUMBER:
FILING DATE:
FOR APPLICATION TO WOMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/09010715
Patent No. 6146625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68.9%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1: 441 amino acids amino acid
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Best Local Similarity 71.4.

Best Local Similarity 71.4.
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185 SATYYFK 191
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US-09-010-715-8
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Sequence 8, Application US/09328474

Patent No. 6045794

GENERAL INFORMATION:
APPLICANT: Cousens, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Edray, Patrick W.
APPLICANT: La Trong, Hai
APPLICANT: Tjoelker, Larry W.
APPLICANT: Tjoelker, Larry W.
TITLE OF INVENTION: Platelet-Activating Factor
TITLE OF INVENTION: Acetylhydrolase
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 31; DB 3; Length 441;
Pred. No. 2e+02;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Rclease #1.0, Version #1.25
APPLICATION NUMBER: US/09/328,474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/483,232
FILING DAME: U7-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
ATTORNEY/AGENT INFORMATION:
NAME: RID-LAUGE, LI-H915en
RECIESTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 27866/34026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                   STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
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Eberhardt, Christine D.
Gray, Patrick W.
Le Trong, Hai
fjoelker, Larry W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68.9%;
71.4%;
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Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-09-328-474-8
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CITY: Chicago
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185 SATYYFK 191
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Gaps

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68.9%; Score 31; DB 4; Length 441; 71.4%; Pred. No. 2e+02; Live 2; Mismatches 0; Indels
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/010,715
FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-COT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 6203790and, Greta E.
REGISTRATION NUMBER: 35,302
REGISTRATION NUMBER: 27866/32793
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION 1NFORMATION:
TELEFORMUNICATION 1NFORMATION:
TELEFORMUNICATION 1NFORMATION:
TELEFORMUNICATION ON SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 68.9
Best Local Similarity 71.4
Matches 5; Conservative
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; MOLECULE TYPE: protein
US-09-577-758-8
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185 SATYYFK 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 31; DB 4; Length 441;
Pred. No. 2e+02;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cousens, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: Gray, Hai
APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor
TITLE OF INVENTION: Acetylhydrolase
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,715
                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION DATE:
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
PRIOR APPLICATION DATE: US 08/133,803
FILING DATE: 06-OCT-1993
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6146672404, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 37,302
REFERENCE/DOCKET NUMBER: 35,302
RELECOMMUNICATION INFORMATION:
TELEFAX: (312) 474-6300
TELEFAX: (312) 474-6448
INFORMATION FOR SEQ. ID NO: 8:
SECHENCE CLARAR PROFESSION IN OR: 8:
       United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/09577758; Patent No. 6203790; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
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Best Local Similarity 71.4
Matches 5; Conservative
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185 SATYYFK 191
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US-09-577-758-8
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on:

July 1, 2002, 16:20:37; Search time 46.58 Seconds (without alignments) 24.755 Million cell updates/sec

US-09-461-061A-3 56

Perfect score:

1 IDNVKKARVQVV 12 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283138 seqs, 96089334 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

pir1:\* pir2:\* pir3:\* pir4:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	kininoqen, LMW pre	HMM	L.MW	kininogen, LMW I p	kininogen, HMW II	HMW	-comp	hypothetical prote		major acute phase	T-kininogen I prec	፞	T-Kininogen, LMW I	K-kininogen, LMW I	kininogen, HMW I p	regulatory protein	hydrogenase (EC 1.	sortase homolog lm	sortase homolog li	hypothetical prote	conserved hypothet	branched-chain ami	conserved hypothet	probable ferredoxi	hypothetical prote		t-complex-type mol	hypothetical prote	endopeptidase [imp
SUMMARIES	ID	KGHUL1	KGHUH1	KGBOL2	KGBOL1	KGBOH2	KGBOH1	A71610	G71103	AH1085	KGRTM	KGRTT1	A23897	B28055	A28055	A25486	RGBYC3	D57150	AI1190	AI1548	F72216	C95272	S14619	A99409	C75513	T33626	C87388	S57083	AF1449	F89819
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hypothetical prote	fatty-acid synthas	ATP synthase B cha	auxin-induced prot	vacuolar atp synth	hypothetical prote	heat shock protein	glycerophosphodies	hypothetical prote	hypothetical prote	toxic anion resist	hypothetical prote	paramyosin - nemat	aspartate transami	aconitate hydratas	argininetRNA lig
T49279	T18200	E71709	T10885	T37535	S23538	S74373	G75217	A64142	н87293	B69757	H71191	B44972	A47094	C64362	F64329
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881	2342	158	203	227	246	249	250	262	264	363	380	389	400	424	266
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35	32	34	34	34	34	34	34	34	34	34	34	34	34	34	34
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

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SULT	HUL1

Kuhinogen, LMW precursor [validated] - human
NiAlternate names: alpha-2-thiol proteinase inhibitor; preprokininogen
NiContenias: bradykinin (kalidated)
NiContenias: bradykinin (kalidated)
C;Decies: Homo sapiens (man)
R;Othubo, I: Kurachi, K.; Takasawa, T.; Shiokawa, H.; Sasaki, M.
Biochemistry 23, 5691-5697, 1984
A;Title: Isolation of a human cDNA for alpha-2-thiol proteinase inhibitor and its ide
A;Reference number: A90490; MUD:85122621
A;Accession: A01280
A;Residues: 11-427 COHK>
A;Cross-references: GB:K02566; NID:g177889; PIDN:AAA35497.1; PID:g177890
B;Takagaki, Y.; Kitamura, N.; Nakanishi, S.
J: Biol. Chem. 260, 8601-8609, 1985
A;Title: Cloning and sequence analysis of cDNAs for human high molecular weight and I
A;Recession: B2576
A;Molecule type: mRNA
A;Residues: 11-427 CTMA
A;Recience number: A92544; MUD:85234582
A;Cross-references: GB:MU1437; NID:g186751; PIDN:AAB59551.1; PID:g386853
A;Cross-references: GB:MU1437; NID:g186751; PIDN:AAB59551.1; PID:g386853
A;Cross-references: GB:MU1437; NID:g186751; PIDN:AAB59551.1; PID:gamm, N
A;Title: Amino acid sequence of the light chain of human low molecular mass kininogen
A;Reference number: A27900
A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;Molecule type: A;M

A Molecule type: protein

A Residues: 390-427 (LOT>

A Residues: 390-427 (LOT>

B Mondrou, T.; Carretero, O.A.; Proud, D.; Walz, D.; Scicli, A.G.

B Mondrou, T.; Carretero, O.A.; Proud, D.; Walz, D.; Scicli, A.G.

B Mochem. Biophys. Res. Commun. 152, 519-526, 1988

A Fiftle: A new Kinin molety in human plasma kininogens.

A; Reference number: A27699; MUID:88209021

A; Reference number: A27699; MUID:88209021

A; Residues: 380-389 < MIN>

B; Maeda, H.; Matsumura, Y.; Kato, H.

J. Biol. Chem. 263, 16051-16054, 1988

A; Title: Purification and identification of (hydroxyprolyl(3)) bradykinin in ascitic for the control of the control

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A;Wolecule type: protein A;Residues: 381-389 <MAE> R;Sasaguri, M.; Ikeda, M.; Ideishi, M.; Arakawa, K. Biochem. Biophys. Res. Commun. 150, 511-516, 1988 A;Title: Identification of [Mydroxyproline(3)]-lysyl-bradykinin released from human A;Reference number: A34030; MUID:88106632

A; Molecule type: protein A; Residues: 380-389 <SAS>

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A; Molecule type: mRNA
A; Residues: 'ANSM',253-377 <AUE>
A; Note: differences are due to known cloning artifacts
A; Note: differences are due to known cloning artifacts
B; Lottspeich, F; Kellermann, J; Henschen, A.; Foertsch, B.; Muller-Esterl, W.
Eur. J Biochem. 152, 307-314, 1985
A; Title: The amino acid sequence of the light chain of human high-molecular-mass kini
A; Reference number: A91153; MUID:86030270
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A;Residues: 380-389 <MIN>
R;Maeda, H.; Matsumura, Y.; Kato, H.
5;Maeda, H.; Matsumura, Y.; Kato, H.
J. Biol. Chem. 263, 16051-16054, 1988
A;Title: Purification and identification of [hydroxyprolyl(3)]bradykinin in ascitic f
A;Reference number: A31905; MUID:89034061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein
A; Residues: 379-644 (LOTA)
A; Note: the bradykinin sequence preceding the light chain sequence was not determined
A; Note: the bradykinin sequence preceding the light chain sequence was not determined
R; Kellermann, J; Lottspeich, F.; Henschen, A.; Mueller-Esterl, W.
Eur. J. Blochem. 154, 471-478, 1986
Eur. J. Blochem. 154, 471-478, 1986
A; Ritle: Completion of the primary structure of human high-molecular-mass kininogen.
A; Reference number: A24871; MUID:86108361
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A; Residues: 381-389 <MAE>
R; Sasaguri, M.; Ikeda, M.; Ideishi, M.; Arakawa, K.
Biochem. Biophys. Res. Commun. 150, 511-516, 1988
A; Title: Identification of [hydroxyproline(3)]-lysyl-bradykinin released from human p
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in Kinins IV, Greenbaum, L.M., and Margolius, H.S., ed., pp.85-89, Plenum Press, New
A;Title: Amino acid sequence of the light chain of human high molecular mass kininoge
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A; Residues: 1-19;189-192;310-314;381-389 <LEN1>
K; Kato, H.; Matsumura, Y.; Maeda, H.
FEBS Lett. 232, 252-254, 1988
A; Title: Isolation and identification of hydroxyproline analogues of bradykinin in hu
A; Reference number: A61495; MUID:88211869
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A;Molecule type: protein
A;Residues: 380-389 <58AS-
R;Lenarcic, B.; Gabrijelcic, D.; Rozman, B.; Drobnic-Kosorok, M.; Turk, V.
Biol. Chem. Hoppe-Seyler 369, 257-261, 1988
A;Tille: Human cathepsin B and cysteine proteinase inhibitors (CPIs) in inflammatory
A;Reference number: S02482; MUID:89076517
                                                   FEBS Lett. 321, 93-97, 1993
A;Title: Cloning, expression and characterization of human kininogen domain
A;Reference number: S32422; MUID:93223854
     D.; Mentele, R.; Assfalg-Machleidt, I.
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A; Residues: 379-389, K',390-407,'Q',409-644 <KEL2>
R; Mindroiu, T.; Carretero, O.A.; Proud, D.; Walz, D.; Scicli, A.G.
Biochem. Biophys. Res. Commun. 152, 519-526, 1988
A; Title: A new kinin monety in human plasma kininogens.
A; Reference number: A27699; MUID:88209021
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A; Residues: 'Z', 20-380 <KEL1>
           R; Auerswald, E.A.; Roessler,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: urine
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A,Residues: 381-389 <KAT2>
A,Experimental source: urine
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A; Residues: 380-389 < KAT1>
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F.142-253/Domain: Cystatin homology <CY2>
F.244-375/Domain: Cystatin homology <CY2>
F.264-375/Domain: Cystatin homology <CY3>
F.380-380/Product: 1ysyl-bradykinin (Kallidin II) #status experimental <BDY>
F.380-380/Product: DAW kininogen light chain #status experimental <LCH>
F.381-389/Product: LMW kininogen light chain #status experimental <LCH>
F.390-427/Product: LMW kininogen light chain #status experimental <LCH>
F.390-427/Product: LMW kininogen light chain #status experimental <LCH>
F.380-407,83-94,107-126,142-145,206-218,229-248,264-267,328-340,351-370/Disulfide bonds: F.48,169,205,294/Anding site: carbohydrate (Asn) (covalent) #status predicted F.393-380/Cleavage site: Met-Lys (kallikrein) #status experimental F.383-390/Cleavage site: Arg-Ser (kallikrein) #status experimental F.389-390/Cleavage site: Arg-Ser (kallikrein) #status experimental F.389-390/Cleavage site: Arg-Ser (kallikrein) #status experimental F.481/Flibiding site: carbohydrate (Thr) (covalent) #status absent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cysteine proteinase inhibitor; glyd
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C; Date: 28 May-1986 #sequence_revision 28.
C; Date: 28 May-1987 #sequence_revision 28.
C; Date: 28.
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V. Biol. Chem. 260, 8601-8609, 1985
A;Title: Cloning and sequence analysis of CDNAs for human high molecular weight and low
A;Reference number: A92544; MUID:85234582
                                                                                                                 kininogen gene and a model for its evolut:
                                                                                                                                                                                                                                                                                                                                                                           A)Title: Structural features of plasma kinins and kininogens.

A)Reference number: A91455, MUID:90255622

A)Contents: annotation; bradykinin

C)Comment: The LAW kininogen precursor is produced from the same gene as the HWW form (C)Comment: Kininogen is a cysteine proteinase inhibitor, takes part in initiation of the C)Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator, xyproline residue is present in the kininogen prior to the release of bradykinin.
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N;Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen; prokininogen
N;Contains: bradykinin (kallidin I); HMW kininogen I; HMW kininogen II; low molecular
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R;Kitamura, N.; Kitagawa, H.; Fukushima, D.; Takagaki, Y.; Miyata, T.; Nakanishi, J. Biol. Chem. 260, 8610-8617, 1985
A;Title: Structural organization of the human kininogen gene and a model for its A;Reference number: A92545; MUID:85234583
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A;Introns: 65/3; 102/3; 131/1; 188/3; 224/3; 253/1; 310/3; 346/3; 375/3; 401/3
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A;Cross-references: GB:M11437; NID:g186751; PIDN:AAB59550.1; PID:g386852
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C; Keywords: alternative splicing; blood coagulation; cysteine protein
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-389,390-427/Product: LMW prokininogen (kininogen I) #status predicted <F;19-389,390-427/Product: LMW kininogen II #status predicted <MAT2>
F;19-389,79roduct: LMW kininogen heavy chain #status predicted <HCH>
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100.0%; Pred. No. 0.011;
ive 0; Mismatches 0;
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A;Cross-references: GDB:125256; OMIM:228960
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A;Residues: 1-389 <OHK>
A;Cross-references: GB:K02566; NID:g177889
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Best Local Similarity 100.
Matches 12; Conservative
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F.244-375/Domain: cystatin homology <cr2>
F.244-375/Domain: cystatin homology <cr2>
F.244-375/Domain: cystatin homology <cr3>
F.380-380/Product: lysyl-bradykinin (kallidin I) #status experimental <br/>F.380-380/Product: bradykinin (kallidin I) #status experimental <br/>F.381-389/Product: bradykinin (kallidin I) #status experimental <br/>F.390-644/Domain: HWW kininogen light chain #status experimental <cr>
F.381-389/Product: low molecular weight growth promoting factor #status experiments<br/>F.19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experiment<br/>F.18-614,83-94,107-126,142-145,206-218,229-248,264-267,328-340,351-370/Disulfide bonds:<br/>F.18-614,83-94,107-126,142-145,206-218,229-248,264-267,328-340,351-370/Disulfide bonds:<br/>F.169,205,294/Binding site: carbohydrate (Asn) (covalent) #status experimental<br/>F.389-380/Cleavage site: Het-Lys (kallikrein) #status experimental<br/>F.389-380/Cleavage site: Arg-Ser (kallikrein) #status experimental<br/>F.389-380/Cleavage site: Arg-Ser (kallikrein) #status experimental<br/>F.389-380/Cleavage site: arbohydrate (Ser) (covalent) #status experimental<br/>F.381-340,5557,571,593,628/Binding site: carbohydrate (Ser) (covalent) #status experimental
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A/IDSSTILLS inclusion: 3427-3427
A/Introns: 65/3; 102/3; 131/1; 188/3; 224/3; 253/1; 310/3; 346/3; 375/3
C/Superfamily: kininogen; cystatin homology
C/Superfamily: kininogen; cystatin homology
C/Seywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; dupl
F;1-18/Domain: signal sequence #status experimental <SIG>
F;19-18/Domain: signal sequence #status experimental <Br/>F;19-379,390-644/Product: HMW kininogen II #status experimental <MATI>
F;19-379,0main: HMW kininogen ineavy chain #status experimental <HCH>
F;19-11/Domain: cystatin homology <CNI>
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A; Residues: 431-434 <STR>
A; Residues: 431-434 <STR>
R; Kitaguaw, N.; Kitaguaw, H.; Fukushima, D.; Takagaki, Y.; Miyata, T.; Nakanishi, S.
J. Biol. Chem. 260, 8610-8617, 1985
A;Title: Structural organization of the human kininogen gene and a model for its evoluti
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A;Title: Structural features of plasma kinins and kininogens.
A;Reference number: A;1455; MID:90255622
A;Contents: annotation; bradykinin
C;Comment: The HMW kininogen precursor and the LMW form are produced from the same gene C;Comment: Kininogen is a cysteine proteinase inhibitor, takes part in initiation of the C;Comment: The glycine/histidine/lysine-rich region of HWW kininogen light chain is impo C;Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator, is xyproline residue is present in the kininogen prior to the release of bradykinin.
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XResidues: 450-452, 7x',454,7x',456 <LIT>
R;Straczek, J; Maachl, F; le Nguyen, D.; Becchi, M.; Heulin, M.H.; Nabet, P.; Bellevil
FEBS Lett. 373, 207-211, 1995
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A; Molecule type: protein
A;Residues: 380-389 cKAT3.
K;Lenarcic, B.; Krasovec, M.; Ritonja, A.; Olafsson, I.; Turk, V.
FEBS Lett. 280, 211-215, 1991
A;Title: Inactivation of human cystatin C and kininogen by human cathepsin I
A; Reference number: S14303; MUID:91192133
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Blochem. J. 307, 341-346, 1995
Aritile: Human mast cell tryptase isoforms: separation and
AkReference number: S55239; MUID:95251593
AkAccession: S55239
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                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein
A; Residues: 264-359, 'N', 361-375 <LEN2>
R; Little, S.S.; Johnson, D.A.
Biochem. J. 307, 341-346, 1995
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Best Local Similarity
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C;Dates 14.007.1983 #Sequence_revision 14-Nov-1983 #text_canage 28-may-1999
C;Datession: A01284
R;Nawa, H.; Kitamura, N.; Hirose, T.; Asai, M.; Inayama, S.; Nakanishi, S.
Proc. Natl. Acad. Sci. U.S.A. 80, 90-94, 1983
A;Title: Primary structures of bovine liver low molecular weight kininogen precursors A;Reference number: A93984; MUID:83117859
A;Reference number: A93984; MUID:83117859
A;Residues: 1-434 ANAW
A;Residues: 1-434 ANAM
A;R
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R; Nawa, H.; Kitamura, N.; Hirose, T.; Asai, M.; Inayama, S.; Nakanishi, S.
Proc. Natl. Acad. Sci. U.S.A. 80, 90-94, 1983
A; Title: Primary structures of bovine liver low molecular weight kininogen precursors A; Reference number: A93984; MUID:83117859
A; Accession: A01283
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Kininogen, LMW II precursor - bovine
N'Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen
N'Contains: bradythin (kallidin); Kininogen I; kininogen II; prokininogen
C;Species: Bos primigenius taurus (cattle)
C;Species: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 28-May-1999
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C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 22-Jun-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 434;
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; Mismatches
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83.3%;
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Best Local Similarity 83.3
Matches 10; Conservative
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A; Residues: 1-436 <NAW>
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Gaps

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100.0%; Score 56; DB 1; Length 644; larity 100.0%; Pred. No. 0.017; Conservative 0; Mismatches 0; Indels

Tue Jul

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Score 44;
Pred. No. 3
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J. Biochem. 67, 313-323, 1970
    Biochem. 152, 307-314, 1985
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83.3%;
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A; Residues: 378-393 <KAT>
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Best Local Similarity
Matches 10; Conserv
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                         Kininogen, HWW II precursor - bovine
N'Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen
N'Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen
N'Contains: bradykinin (kallidhn); kininogen I; kininogen II; prokininogen
C'Species: Bos primigenius taurus (cattle)
C'Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 22-Jun-1999
C'Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 22-Jun-1999
C'Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 22-Jun-1999
R'Kitamura, N: Takagaki, Y: Furuto, S: Tanaka, T:: Nawa, H:: Nakanishi, S.
Natitle: A single gene for bovine high molecular weight and low molecular weight kininog
A'Reference number: A93317; MUID: 84014106
A'Rocession: A01282
A'Molecule type: mRNA
A'Residues: 1-619 < KITA
A'Residues: 1-619 & KI
C; Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; glyd
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A; Reference number: A91923; MUD: 70180420
A; Accession: A91923
A; Residues: 375-391 «KAT>
A; Residues: 375-391 «KAT>
B; Residues: 375-391 «KAT>
A; Title: Rimar Y.N.; Rato, H.; Iwanaga, S.; Suzuki, T.
J. Biochem. 79, 1201-1222, 1376
A; Title: Primary structure of bovine plasma high-molecular-weight kininogen. The amino a A; Reference number: A91941; MUD: 76260155
A; Accession: A91941
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A;Reference number: A91938; MUID:75170265
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A; Residues: 456-496 <HA2>
R; Sueyoshi, T.; Miyata, T.; Hashimoto, N.; Kato, H.; Hayashida, H.; Miyata, T.; Iwanaga,
J. Blol. Chem. 262, 2768-2779, 1987
A; Title: Bovine high molecular weight kininogen. The amino acid sequence, positions of c
A; Reference number: A92627; MUID:87137530
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A;Residues: '2',20-104,'E',106-256,'XX',257-376 <SUE>
R;Lottspeich, F.; Kellermann, J.; Henschen, A.; Foertsch, B.; Muller-Esterl, W.
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A; Residues: 387-455 < HAN>
A; Note: 398-Pro, 401-Val, and 455-Lys were also found
K; Han, Y.N.; Komlya, M.; Iwanaga, S.; Suzuki, T.
J. Blochem. 77, 55-68, 1975
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A.Reference number: A94300
A.Contents: annotation; disulfide bonds
A.Note: article in Japanese
A.Note: article in Japanese
C.Comment: The HWW kininogen precursor is produced from the same gene as the LWW form
C.Comment: The BWW kininogen is a cysteine proteinase inhibitor, takes part in initiation of
C.Comment: Rininogen is a cysteine proteinase inhibitor, takes part in initiation of
C.Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator
C.Comment: Bradykinin, released from kininogen prior to the release of bradykinin.
C.Superfamily: kininogen: cystatin homology
C.Keywords: alternative splicing; blod coagulation; cysteine proteinase inhibitor; d
F.1-18/Domain: signal sequence #status predicted <51G>
F:19-619/Product: HWW kininogen II #status predicted <MAT>
F:19-519/Forduct: HWW kininogen II heavy chain #status experimental <HCH>
A;Title: The amino acid sequence of the light chain of human high-molecular-mass kini A;Reference number: A91153; MUID:86030270
A;Contents: annotation; bovine cleavage sites; bovine carbohydrate binding sites R;Sueyoshi, T.; Miyata, T.; Kato, H.; Iwanaga, S. Seikagaku 56, 808, 1984
A;Title: Disulfide bonds in bovine HWW kininogens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;19-130/Domain: cystatin homology <CY1>
F;141-252/Domain: cystatin homology <CY2>
F;241-372/Domain: cystatin homology <CY2>
F;241-372/Domain: cystatin homology <CY3>
F;241-372/Domain: cystatin homology <CY3>
F;377-386/Product: lysyl-bradykinin (kallidin II) #status experimental <RBDY>
F;378-386/Product: hww kininogen II light chain #status experimental <LCH>
F;387-619/Product: Hww kininogen II light chain #status experimental <LCH>
F;188-488/Region: glycine/histidine/lysine-rich
F;279/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experi:
F;27-589,82-93,106-125,141-144,205-217,228-247,261-264,325-337,348-367/Disulfide bond
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F;87,168,169,204,280/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;136/Binding site: carbohydrate (Thr) (covalent) (partial) #status experimental
F;136/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental
F;376-377/Cleavage site: Met-Lys (Kallikrein) #status experimental
F;386-387/Cleavage site: A-hydroxyproline (Pro) #status predicted
F;386-387/Cleavage site: Arg-Ser (Kallikrein) #status experimental
F;396,400,404.510/Binding site: carbohydrate (Ser) (covalent) #status
F;396,520,534,546,551,568/Binding site: carbohydrate (Thr) (covalent) #status
F;496-497/Cleavage site: Arg-Thr (kallikrein) #status experimental
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A;Accession: A91923
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A;Residues: 1-621 <KIT>
A;Cross-references: GB:V01491; GB:K01757; NID:g491; PIDN:CAA24735.1; PID:g492
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Nature 305, 545-549, 1983
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2.9;
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Gaps

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Appointational protein Imco0087 [imported] - Listeria monocytogenes (strain EGD-e)
C;Species: Listeria monocytogenes
C;Species: Charet.
C;Accession: AH1085
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec
C;Domanguez-Bernal, G; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fshli,
D; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.;
A;Authors: Kreft, J.; Kuhn, M.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUD:21537279; PMID:11679669
A;Accession: AH1085
A;Accession: AH1085
A;Accession: AH1085
A;Residues: 1-768 GLA>
A;Residues: 1-768 GLA>
A;Experimental source: strain EGD-e
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C; Date: 14 Aug-1998 #sequence_revision 14-Aug-1998 #text_change 05-Nov-1999
C; Cacesion: (71103
C; Cacesion: (71103
C; Accession: (71103
C; Ac
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A; Residues: 1-309 < KAM>
A; Cross-references: GB: APP000004; NID: 93236131; PIDN: BAA30189.1; PID: d1031132; PID: 932
A; Experimental source: strain OT3
A; Experimental source: strain OT3
A; Note: this accession replaces an interim accession for a sequence replaced by GenBa
                                                                                                                                                                                                                                                                                                                                                                        GB:AE001362; NID:g3845234; PIDN:AAC71916.1; PID:g384
            A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum. A;Reference number: A71600; MUID:99021743
A;Accession: A71610
A;Accession: A71610
A;Actus: preliminary; nucleic acid sequence not shown; translation not shown A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Accession: A540 cdRP>
A;Residues: 1-540 cdRP>
A;Residues: 1-540 cdRP>
A;Residues: 1-540 cdRP>
A;Residues: acidences: clone 3D7
C;Genetics: 
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Pred. No. 13;
5; Mismatches
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Mismatches
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Pred. No.
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54.5%;
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66.7%;
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Best Local Similarity
Matches 8; Conserva
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Best Local Similarity
Matches 6; Conserv
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C; Genetics:
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A; Residues: 'Z', 20-133,'I', 125-127,'I', 129-378 <SUE>
A; Residues: 'Z', 20-133,'I', 125-127,'I', 129-378 <SUE>
R; Lottspeich, F:, Kellermann, J:, Henschen, A.; Foertsch, B.; Muller-Esterl, W.
Eur. J. Blochem. 152, 307-314, 1985
A; Title: The amino acid sequence of the light chain of human high-molecular-mass kininog A; Reference number: A91153; MUID: 86030270
A; Contents: annotation; bovine cleavage sites; bovine carbohydrate binding sites
B; Sueyoshi, T.; Miyata, T.; Kato, H.; Iwanaga, S.
Seikagaku 56, 808, 1984
A; Title: Disulfide bonds in bovine HWM kininogens.
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A; Contents: annotation; disulfide bonds
A; Mote: article in Japanese
C; Comment: The HWW kininogen precursor is produced from the same gene as the LWW form as C; Comment: The HWW kininogen precursor is produced from the same gene as the LWW form as C; Comment: The HWW kininogen is a cysteine proteinase inhibitor, takes part in initiation of the C; Comment: The glycine/histidine/lysher-rich region of HWW kininogen light chain is impo C; Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator, i xyproline residue is present in the kininogen prior to the release of bradykinin.
C; Superfamily: kininogen: cystatin homology
C; Reywords: alternative splicing; blood coaquiation; cysteine proteinase inhibitor; dupl F; 1-18/Domain: signal sequence #status predicted <a href="Milliongen">MILLIONGENTED MILLIONGENTED MILLIONGENTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Biochem. 77, 55-68, 1975
A;Title: Studies on the primary structure of bovine high-molecular-weight kininogen. Ami A;Reference number: A91938; MUID:75170265
                                                                                                                                                                                                                                                                                          A; Wolecule type: protein

R; Residuce: 458-498 < 4Hn.>
R; Residuce: 458-498 < 4Hn.>
R; Residuce: 458-498 < 4Hn.>
R; Sueyoshi, T.; Miyata, T.; Hashimoto, N.; Kato, H.; Hayashida, H.; Miyata, T.; Iwanaga, J. Biol. Chem. 262, 2768-2779, 1987
J. Biol. Chem. 262, 2768-2779, 1987
A; Title: Bovine high molecular weight kininogen. The amino acid sequence, positions of GA; Reference number: A92627; MUID:87137530
A; Accession: A29559
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Pred. No. 2.9;
); Mismatches
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83.3%;
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A; Molecule type: protein
A; Residues: "C; 20-48;376-430 <ENJ>
A; Residues: "S: Sugiyama, K.; Takahashi, M.; Shumiya, S.; Tomino, S.; Nagase, S.
Jpn. J. Cancer Res. 81, 63-68, 1990
A; Title: Identification of a protein increasing in serum of Nagase analbuminemic rats
A; Reference number: PL0193; MUID:90216390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Molecule type: DNA
A;Residues: 1-60, E', 62-113, 'R', 115-165, 'F', 167-178, 'TKI', 182-211, 'F', 213-256, 'S', 258
A;Residues: 1-60, E', 62-113, 'R', 115-165, 'F', 167-178, 'TKI', 182-211, 'F', 213-256, 'S', 258
A;Regrama, R.; Kitamura, N.; Oktubo, H.; Nakanishi, S.
J. Biol. Chem. 262, 2345-2351, 1987
A;Reference number: 262, 2345-2351, 1987
A;Reference number: A25488; MUID:87137465
A;Reference number: A25488
A;Recession: B25488
A;Status: preliminary
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A; Residues: 1-48 < KAGS
A; Cross-references: GB:M4356; NID:g205090; PIDN:AAA41492.1; PID:g205091
A; Cross-references: GB:M14356; NID:g205090; PIDN:AAA41492.1; PID:g205091
B; Enjyoji, K.; Kato, H.; Hayashi, I.; Oh-ishi, S.; Iwanaga, S.
J. Biol. Chem. 263, 965-972, 1988
A; Title: Purification and characterization of two kinds of low molecular weight kinin
A; Reference number: A28525; MUID:88087225
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C; Superfamily: kininogen; cystatin homology
C; Superfamily: kininogen; cystatin homology
C; Superdicted <516>
F; 1-18/Domain: signal sequence #status predicted <516>
F; 19-430/Product: T-kininogen I #status experimental <MAT>
F; 19-130/Domain: cystatin homology <CX1>
F; 19-130/Domain: cystatin homology <CX2>
F; 263-374/Domain: cystatin homology <CX3>
F; 378-386/Product: bradykinin #status predicted 
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A;Residues: 340-430 <SIE>
A;Residues: 340-430 <SIE>
A;Experimental source: clone pSG17
C;Comment: At least three types of LMW kininogen precursors are present in rat plasma ceding bradykinin.
                                      R;Enjyoji, K.; Kato, H.; Hayashi, I.; Oh-ishi, S.; Iwanaga, S.
J. Biol. Chem. 263, 973-994, 1988
A;Title: Purification and characterization of rat T-kininogens isolated from plasma
A;Reference number: A92729; MUID:88087226
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A;Residues: 376-430 <BNZ.
R;Sierra, F.; Walter, R.; Vautravers, P.; Guigoz, Y.
Arch. Biochem. Biophys. 322, 333-338, 1995
A;Title: Identification of several isoforms of T-kininogen expressed in the liver
A;Reference number: S68034; MUID:96032652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 330-420, 'R', 422-429,'P' <KAN>
R;Anderson, K.P.; Croyle, M.L.; Lingrel, J.B.
Gene 81, 119-128, 1989
A;Title: Pxinary structure of a gene encoding rat T-kininogen.
A;Reference number: JQ0027; MUID:90034172
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C.Steywords: bradykinin; cystatin homology
C.Steywords: bradykinin; cysteine proteinase inhibitor; duplication; glycoprotein; inflam
C.Steywords: bradykinin; cysteine proteinase inhibitor; duplication; glycoprotein; inflam
C.Steywords: signal sequence (fragment) #status predicted <SIG>
F;12-423/Product: major acute phase alpha-1 protein #status predicted <MAT>
F;12-123/Pomain: cystatin homology <CX1>
F;34-245/Pomain: cystatin homology <CX2>
F;35-367/Pomain: cystatin homology <CX3>
F;31-379/Product: bradykinin #status predicted <BDY>
F;12/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;161,197/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 22-Jun-1999
C;Accession: A01286; D25486; A28526; PL0193; JQ0027; B25488; A28525; S68036
R;Furuto-Kato, S.; Matsumoto, A.; Kitamura, N.; Nakanishi, S.
J. Biol. Chem. 260, 12054-12059, 1985
A;Title: Primary structures of the mRNAs encoding the rat precursors for bradykinin and nhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-423 <COL>
C;Comment: This plasma glycoprotein inhibits cysteine proteinases. During acute inflamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        major acute phase alpha-1 protein precursor - rat (fragment)
N;Conteins: bradykinin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 12-Apr-1996
C;Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 12-Apr-1996
C;Cocsasion: A01285
R;Cole, T; Inglis, A.S.; Roxburgh, C.M.; Howlett, G.J.; Schreiber, G.
FEBS Lett. 182, 57-61, 1985
A;Title: Major acute phase alphal-protein of the rat is homologous to bovine kininogen
A;Reference number: A01285; MUID:85127561
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A; Molecule type: mRNA
A; Residues: 1-430 < F(PN)
B; Kitagawa, H.; Kitamura, N.; Hayashida, H.; Miyata, T.; Nakanishi, S.
J. Biol. Chem. 262, 2190-2198, 1987
A; Title: Differing expression patterns and evolution of the rat kininogen gene family. A; Reference number: A92625; MUID:87137443
A; Rocession: D25486
A; Molecule type: DNA
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                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                DB 2;
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N;Contains: bradykinin; T-kinin
                                                                                                                                                        Score 39; DB;
Pred. No. 31;
4; Mismatches
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                                                                                                                                                            69.6%;
63.6%;
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Matches 7; Conservative
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Matches 9; Conserv
                                      A;Gene: 1mo0087
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C; Genetics
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C; Accession: A28055
F; Furuto-Nato, S.; Matsumoto, A.; Kitamura, N.; Nakanishi, S.
J. Biol. Chem. 260, 12054-12059, 1985
A; Title: Primary structures of the mRNAs encoding the rat precursors for bradykinin a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nicontains: bradyfinin
C;Species: Rattus norvegicus (Norway rat)
C;Date: Ober 1989 #sequence_revision 08-Mar-1989 #text_change 15-Nov-1996
C;Accession: A25486
R;Kitagawa, H.; Kitamura, N.; Hayashida, H.; Miyata, T.; Nakanishi, S.
J. Biol. Chem. 262, 2190-2198, 1987
A;Title: Differing expression patterns and evolution of the rat kininogen gene family A;Reference number: A92625; MUID:87137443
  F;263-374/Domain: cystatin homology <CY3>
F;19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experi: F;82,126,168,204,326/Binding site: carbohydrate (Asn) (covalent) #status predicted F;83-94,107-125,141-144,205-217,228-247,263-266,327-339,350-369/Disulfide bonds: #sta
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Jun-1989 #sequence_revision 20-Jun-1989 #text_change 15-Nov-1996
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A; Residues: 1-639 < KIT>
A; Residues: 1-639 < KIT>
A; Note: the authors translated the codon CAA for residue 347
C; Superfamily: kininogen; cystatin homology
C; Superfamily: kininogen; cystatin homology
F; 1-18/Domain: signal sequence #status predicted <SIG>
F; 1-9-539/Product: kininogen, HMW I #status predicted <MAT>
F; 19-131/Domain: cystatin homology <CYI>
F; 142-253/Domain: cystatin homology <CYI>
F; 264-375/Domain: cystatin homology <CXI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: A28055
A; Molecule type: mRNA
A; Residues: 1-433 <FUR>
C; Superfamily: kininogen; cystatin homology
C; Keywords: alternative splicing
F; 1-18/Domain: signal sequence #status predicted <SIG>F; 19-433/Product: K-kininogen, LMW I #status predicted
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Pred. No. 27;
0; Mismatches
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Pred. No. 27;
0; Mismatches
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40;
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Pred. No.
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75.0%;
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75.08;
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75.08;
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Best Local Similarity
Matches 9; Conserv
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A; Residues: 5-430 cAND2>
A; Cross-references: GB-M11661; NID:g205307; PIDN:AAA41570.1; PID:g205308
A; Note: the authors translated the codon CTC for residue 410 as Arg, CTA for residue 415
C; Superfamily: Kininogen; cystatin homology
F:19-130/Domain: cystatin homology cCTL>
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Jun-1989 #sequence_revision 20-Jun-1989 #text_change 12-Dec-1997
C;Accession: B28055; E25486; B28526; C28526
R;Furuto-Kato, S.; Matsumoto, A.; Kitamura, N.; Nakanishi, S.
J. Biol. Chem. 260, 12054-12059, 1985
A;Tille: Primary structures of the mRNAs encoding the rat precursors for bradykinin and
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A; Molecule type: DNA
A; Residues: 375-430 < KIT>
B; Enjyoji, K.; Kato, H.; Hayashi, I.; Oh-ishi, S.; Iwanaga, S.
B; Enjyoji, K.; Kato, H.; Hayashi, I.; Oh-ishi, S.; Iwanaga, S.
J. Blol. Chem. 263, 973-979, 1988
A; Title: Purification and characterization of rat T-kininogens isolated from plasma of A; Reference number: A92729; MUID:88087226
A; Accession: B28526
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A; Residues: 1-430 cFUR>
R; Kitagawa, H.: Kitamura, N.; Hayashida, H.: Miyata, T.: Nakahishi, S.
Biol. Chem. 262, 2190-2198, 1987
A; Title: Differing expression patterns and evolution of the rat kininogen gene family.
A; Reference number: A92625; MUID:87137443
                                                                                                                                                                                                                             C; Accession: A23897; B23897
R; Anderson, K.P.; Heath, E.C.
J. Biol. Chem. 260, 12065-12071, 1985
A; Title: The relationship between rat major acute phase protein and the kininogens.
A; Reference number: A23897; MUID:86008266
A; Accession: A23897
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                                                                                                                                                                          C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 20-Aug-1999
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A) Residues: E',20-48;376-388, R',390-419, ER',422-430 <EN2>
C) Superfamily: kininogen; cystatin homology
C) Superfamily: kininogen; cystatin homology
C) Keywords: glycoprotein; pyroglutamic acid
E;1-18/Domain: signal sequence #status predicted <SIG>
E;19-430/Product: T-kininogen, LmW II #status experimental <MAT>
E;19-130/Domain: cystatin homology <CX1>
E;141-252/Domain: cystatin homology <CX2>
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27;
                                                                                                                                               major acute phase alpha-1 protein (version 2) - rat
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A;Residues: 'E',20-25,'MD',28-48,376-430 <ENJ>
A;Accession: C28526
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Pred. No.
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75.0%;
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300 IDTVKKATSQVV 311
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Best Local Similarity
These 9; Conserve
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A; Residues: 1-14 <AND1>
A; Accession: B23897
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Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 IDNVKRARVQVV 12 || || || || || Db 301 IDTVKRATSQVV 312 Search completed: July 1, 2002, 16:20:38 Job time: 202 sec

Q9p411 candida alb Q9h6e8 homo sapien Q961x0 homo sapien Q9frt7 arabidopsis O22479 santalum al

Q9pp86 campylobact

Q9TLE3 Q98PT0 Q9PPZ5 Q9UED4

10 110 110 110 110 8

022479 09PP86 910860

081960

051327 098788

Q96q16 mycoplasma Q911a3 dpplycosia Q911a3 dpplycosia Q98pt0 mycoplasma Q9bed4 homo sapien O51327 borrelia bu O59788 sphyrosperm Q95q11 dpplycosia Q95q8 diplycosia 
091uy9 human immun 092998 homo sapien 092770 homo sapien 096fc9 homo sapien 098x98 arabidopsis 045433 caenorhabdi

095GL1 095GK8 095GK8 095GK9 098786 092498 092998 092998 092770 092770

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01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MAJOR ACUTE PHASE ALPHA-1 PROTEIN PRECURSOR (FRAGMENT).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-85127561; PubMed-2578992;
MEDLINE-85127561; PubMed-2578992;
Cole T., Inglis A.S., Roxburgh C.M., Howlett G.J., Schreiber G.;
Cole T., Inglis A.S., Roxburgh C.M., Howlett G.J., Schreiber G.;
Major acute phase alphal-protein of the rat is homologous to bovine kininogen and contains the sequence for bradykinin: its synthesis is regulated at the mRNA level.";
FEBS Lett. 182:57-61(1985).
EMBL; KO2814; AAA41569.1;
InterPro; IPR000010; Cystatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cole T., Inglis A., Nagashima M., Schreiber G.; "Major acuter-phase alpha(1)-protein in the rat: Structure, molecular cloning, and regulation of mRNA levels."; Biochem. Biophys. Res. Commun. 126:719-724(1985).
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Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cystatin_C_M; 1.
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MEDLINE-85149311; PubMed=2579644;
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ProDom; PB001231; cystatin_C_M
SMART; SM00043; CY; 3.
PROSITE; PS00287; CYSTATIN; 2.
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                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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sp_human:*
sp_invertebrate:*
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Matches 20; Conserv
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    NCBI_TaxID=10090;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ADULT FEMALE PLACENTA CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
CLANE:1600027101, FULL INSERT SEQUENCE.
BUNS musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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                                                                                                                                         61.5%; Score 99; DB 11; Length 423; llarity 64.5%; Pred. No. 9.2e-06; Conservative 4; Mismatches 7; Indels
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                                                          POTENTIAL.
F9E8BD3198547949 CRC64;
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(TrEMBLrel. 19, Last annotation update)
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EMBL; M29090; AAA42251.1; -
EMBL; M29083; AAA42251.1; -
EMBL; M29084; AAA42251.1; JOINED.
EMBL; M29081; AAA42251.1; JOINED.
EMBL; M29081; AAA42251.1; JOINED.
EMBL; M29085; AAA42251.1; JOINED.
EMBL; M29085; AAA42251.1; JOINED.
EMBL; M29088; AAA42251.1; JOINED.
EMBL; M29089; AAA42251.1; JOINED.
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INTEFPO: IPR0001010; Cystatin.
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Arakawa T., Aizawa K., Akahira S., Akimura T., Aono H., Arai A.,
A Arakawa T., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
A Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kado H., Kawai J., Kojima Y.,
A Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A.,
Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T.,
A wa C., Saito H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D.,
A bibata K., Shibata Y., Shinagawa A., Shiraki T., Sogabe Y.,
Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y.,
Toya T., Yamamura T., Yasuhishi A., Yoshida K., Yoshino M.,
Muramatsu M., Hayashizaki Y.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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SETRAIN-C57BL/G1; TISSUE-PLACENTA;
MEDLINE-20499374; PubMed-11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length subtraction of cap-trapper prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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STRAIN-CSPELL6J; TISSUE-PLACENTA;
STRAIN-CSPELL6J; PubMed-11076861;
Shibata K., Itch M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itch M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegani T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RIKEN integrated sequence analysis (RISA) system-384-format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIKEN FANTOM Consortium.; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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Genome Res. 10:1757-1771(2000).
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64.5%; Pred. No. 1.3e-05;
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MEDLINE-99279253; Pubmed-10349636;
Carninci P., Hayashizaki Y.;
High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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MEDLINE=21085660; PubMed=11217851;
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(TrEMBLrel. 13, I
(TrEMBLrel. 19, I
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SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-AB972;
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                                                                                                                                                                                                                                                                                                     003984;
                                                                                                                                                                                                                                                                                       003984
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Q03984
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                  Functional annotation of a full-length mouse cDNA collection.";
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Pred. No. 0.73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12; Indels
                                                                                                                 "A novel cystatin-like metastasis associated gene.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00043; CY; 1.
SEQUENCE 167 AA; 18847 MW; 61F776D8445095FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL PROTEIN SPY1252.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  446 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
MURÎNE CMAP (CYSTATIN F) (LEUKOCYSTATIN).
MURINE CMAP OR CST7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-SF370 / ATCC 700294 / SERCTYPE M1;
MEDLINE-21192684; PubMed=11296296;
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                                                                                                     Morita M., Arakawa H., Yoshiuchi N.;
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SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-EMBRYO;
MEDLINE-2108566J; Pubmed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI11298217; Cst7.
InterPro; IPR00010; Cystatin.
InterPro; IPR003243; Cystatin.
Pfam; PF00031; cystatin.1.
Probom; PD001231; Cystatin.C.M; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB015224; BAA34940.1; -. EMBL; AK004420; BAB23298.1; -. HSSP; P01034; 1G96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 48.38;
Matches 14; Consormation
                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                              [1]
SEQUENCE FROM N.A.
                                                                NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Hayashizaki Y.;
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Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.; "Complete genome sequence of an M1 strain of Streptococcus pyogenes."; Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
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Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                        Length 446;
                                                                                                                                                                                                                                                                                                                                               10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Indels
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Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; 246727; CAA86686.1; -.
SGD; SO002587; YDR179W-A.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murphy L., Harris D.E.;
Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                     Hypothetical protein; Complete proteome:
SEQUENCE 446 AA; 51511 MW; F98FB7B071D668A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 protein.
268 Aa; 31096 MW; 45C7F756F36LC71D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 31.1 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAV-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 57.9 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32.6%; Score 52.5; DB 3;
                                                                                                                                                                                                                                                                                        32.9%; Score 53; DB 16; 39.3%; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    268 AA.
                                                                                                                                                                                                                                                                                                                                          7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TLTHTITKLNAENNATFYFKIDNVKKARV 29
                                                                                                                                                                                                                                                                                                                                                                                                 1 TLTHTITKLNAENNATFYFKIDNVKKAR 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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Best Local Similarity 39.33
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 32.6
Best Local Similarity 41.4
Matches 12; Conservative
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TRON N.A.

STRAIN=ATCC 35092 / DSM 1617 / P2;

MEDLINE=2132295; PubMed=11427726;

A She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

A wayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,

A wayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,

A heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medin P.M.K.,

Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

Charlebois R.L., Doolittle W.F., Duguet M., Gassterland T.,

Carrett R.A., Ragan M.A., Sensen C.W., van der Oost J.;

The complete genome of the crenarchaeon sulfolobus solfataricus P2.";

Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).

REMBL; AE006895; AAK431411; ...

RUM Hypothetical protein; Complete proteome.

WHypothetical protein; Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                        Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.
                                                                                       01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
HYPOTHETICAL PROTEIN SSO3039.
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Last annotation update)
                               803 AA.
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STRAIN-BRISTOL N2;
ROblifing T., Wurray J., Antonio B.;
"The sequence of C. elegans cosmid KO8B4.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32.0%; Score 51.5; 31.2%; Pred. No. 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TLTHTITKLNAENNATFYFKIDN-VKKARVQV 31
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01-MAY-2000 (TrEMBLrel. 13, Last seq
                                  PRT;
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K08B4.6 PROTEIN (CYSTATIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 31.2%
Matches 10; Conservative
                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                         Sulfolobus solfataricus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                    NCBI_TaxID=2287;
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                                     ID DTT ACCOUNT OF THE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ΩD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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EMBL; AROE3475, ARO49849.1;
ERBSSE; 3106; M.Aimal.
InterPro; IPR001025; BAH.
InterPro; IPR001525; C5_DNA_meth.
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Rossignol J.-L., Noyer-Weidner M., Vollmayr P., Trautner T.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Fungi, Ascomycota, Pezizomycotina, Pezizomycetes,
Pezizales, Ascobolaceae, Ascobolus.
                                                                                                                                                                                                                                                                                                                                                                                                                          Length 498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: ESSENTIAL FOR DE NOVO METHYLATION AND SEXUAL
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45.8%; Pred. No. 45;
tive 3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Indels
                            Murphy L., Harris D.E.;
Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                              Barrell B., Rajandream M.A.;
Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases
EMBL, 246727; AA886685.1; -
SGD; S0002587; YDR179W-A.
                                                                                                                                                                                                                                                                                                                                60959427D7A230CD CRC64;
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615EDA2F2453C174 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PROBABLE DNA METHYLTRANSFERASE MASC1 (EC 2.1.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 52.5; DB 3;
Pred. No. 36;
5; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     537 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TLTHTITKLNAENNATFYFKIDNVKKARV 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98004231; PubMed=9346245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 HTITKLNAENNATFYFKIDNVKKA 27
                                                                                                                                                                                                                                                                                                 Hypothetical protein. SEQUENCE 498 AA; 57916 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61240 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                          32.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 05, (TrEMBLrel. 05,
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 32.6
Best Local Similarity 41.4
Matches 12; Conservative
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Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ascobolus immersus.
                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                     STRAIN-AB972;
STRAIN=AB972;
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01-JAN-1998
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11; DB 17;

Length 803; Indels ï

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STRAIN-GSS1, DSW 4299 / JCW 9571;
MEDLINE-20570466; PubMed=11121031;
Kawashima T., Amano N., Kolke H., Makino S.-I., Higuchi S.,
Kawashima T., Amano V., Aramaki H., Makino K., Sızuki M.;
Archaeal adaptation to higher temperatures revealed by genomic
sequence of Thermoplasma volcanium.";
Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
EMBL; AP000996; BAB605931; -.
InterPro; IPR001087; Lipase_GDSL.
InterPro; IPR001087; Lipase_GDSL.
Fight Drown 
                                                                                                                 Noelling J., Breton G., Omelohenko M.V., Makarova K.S., Zeng Q., Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I., Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.; Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum."; Bacteriol. 183:4823-4838(2001).

EMBL; AEOG7725; AAR80204.1; ...
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Archaea; Euryarchaeota; Thermoplasmales; Thermoplasmaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31.7%; Score 51; DB 17; Length 92
52.6%; Pred. No. 1.18+02;
.ive 3; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                           62467 MW; 22DB00B060AF6102 CRC64;
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Last annotation update)
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(TrEMBLrel. 19, Last sequence update)
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Pred. No. 61;
1; Mismatches 11
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PROSITE; PS01098; LIPASE_GDSL_SER; UNKNOWN_1.
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                                                                           STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE-21359325; PubMed-11466286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 LTHTITKLNAENNATFYFKIDNVKKARVQV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 31.7%;
Best Local Similarity 46.7%;
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2001 (TrEMBLrel. 18, 01-0CT-2001 (TrEMBLrel. 18, 01-DEC-2001 (TrEMBLrel. 19, TYGIS02957) PROTEIN.
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Best Local Similarity 52.6
Matches 10; Conservative
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SEQUENCE 928 AA;
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Q941Z1;
01-DEC-2001 (
01-DEC-2001 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q978G4;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Malpighiales; Euphorbiaceae; Ricinus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                 Schierack P.S., Lucius R., Sonnenburg B., Hartmann S.A.E.; "Molecular cloning and characterization of Caenorhabditis elegans cystatin D.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clostridium acetobutylicum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 139,
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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STRAIN-CV. CV. SANGUINEUS; TISSUE-COTYLEDON;
Szederkenyi J. Schobert C.;
"CDNA expressed in Ricinus cotyledons.";
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
EMBL: 249697; CAR95971.1;
SEQUENCE 209 AA; 23304 MM; 2E7BBFIDODIDDFFI CRC64;
                                                                                                  Waterston R.; Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                     Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases EMBL; AF100663; AAC68983.1; -. EMBL; AJ310669; CAC33821.1; -.
                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000010; Cystatin.
Pfam: PF00031; cystatin; 1.
SWART; SM00043; CY; 1.
SEQUENCE 139 AA; 15091 MW; 796F1CD81166CEFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         697.1; -. 2E7BBF1D0D1DDFF1 CRC64;
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
011-OCT-ETFIC RECOMBINASE, DNA INVERTASE PIN HOWOLOG
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CYSTEINE PROTEINASE INHIBITOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 51; DB 5;
Pred. No. 15;
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Matches 8; Conservative
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Best Local Similarity
Matches 11; Conserv
                                                  SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
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Q43635;
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                          Oryza sativa (Rice).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Candida albicans (Yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.

NCBI_TaxID=5476;
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                                                                                                                SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBARE;
STRAIN-CV. Matsumoto T., Yamamoto K.;
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC clone:OSJMBa0025P13.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AP003140; BAB55744.1; -.
SEQUENCE 503 AA; 52056 MW; 71DAABBC792DE6E4 CRC64;
                                                                                                                                                                                                                                                                  31.1%; Score 50; DB 10; Length 503; 36.0%; Pred. No. 81; tive 5; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31.1%; Score 50; DB 3; Length 1690; 39.1%; Pred. No. 2.9e+02; ive 5; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ono N., Sudon M.;
"Candida albicans CYR1 gene.";
"Candida albicans CYR1 gene.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB034965; BAA93553.1;
EnterPro; IPR001054; Guanylt_cyclase.
InterPro; IPR001611; LRR_out.
InterPro; IPR001599; LRR_out.
InterPro; IPR0019591; LRR_typ.
InterPro; IPR001932; PP2C_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GUANYLATE_CYCLASES_2; 1.
A; 189400 MW; 8AB32D9B8C747AB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update) PUTATIVE POLYGALACTURONASE-LIKE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1690 AA.
                                                                                                                                                                                                                                                                                                                                               251 TVRGLKVQNSPEFHFRFDNCNGVRV 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00211; guanylate_cyc; 1. Pfam; PF00560; LRR; 16. Pfam; PR00481; PP2C; 2. PRINTS; PR0019; LEURICHRPT. SMART; SM00044; CYCc; 1. SMART; SM00370; LRR; 7. SMART; SM00369; LRR,TYP; 2.
                                                                                                                                                                                                                                                                                                                             5 TITKLNAENNATFYFKIDNVKKARV 29
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                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 36.0%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00332; PP2
SMART; SM00311; PP2
SMART; SM00314; RA;
PROSITE; PS50125; C
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                                                                                      NCBI_TaxID=4530;
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                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
Q9P977
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